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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 26, 2000, 13:15:21 ; Search time 33.21 Seconds

(without alignments)
99.138 Million cell updates/sec

Title: US-09-203-768a-2

Perfect score: 1 MKHLWFFLLVLAAPRWVLSQ.....ARPRHYFDYWGQGLTVYSS 139

Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	622	83.2	116	1 R66324	Human immunoglobulin
2	575.5	76.9	472	1 R31166	Anti-rhesus D reco
3	560.5	74.9	136	1 W24536	Immunoglobulin R6
4	558.5	74.7	123	1 W03757	Anti-rhesus D mono
5	558.5	74.7	142	1 R41285	F105 rearranged va
6	552	73.8	128	1 R12269	Human immunoglobulin
7	550	73.5	116	1 R42689	Vh 71-4. DNA segme
8	541.5	72.4	476	1 W01822	Primate anti-CD4 he
9	541.5	72.4	476	1 W63765	Macaque primatized
10	539	72.1	118	1 R66348	Human immunoglobulin
11	539	72.1	118	1 R66348	Monoclonal antibody
12	539	72.1	118	1 R66348	Human immunoglobulin
13	538	71.9	116	1 R66298	Anti-CD4 cynomolgus
14	536.5	71.7	140	1 W32477	Monkey anti-CD4 he
15	536.5	71.7	140	1 W32477	Anti-CD4 VH peptide
16	536.5	71.7	141	1 R31948	Human gamma-4PE he
17	536.5	71.7	467	1 W14927	Human gamma-4PE he
18	536.5	71.7	467	1 W14925	Human gamma-4E hea
19	536.5	71.7	467	1 W14926	Human gamma-4E hea
20	536	71.7	141	1 W70378	Anti-human CD23 6G
21	533.5	71.2	139	1 W14922	Monkey anti-CD4 he
22	533.5	71.2	139	1 W35284	Monkey anti-human
23	532.5	71.2	139	1 W35988	Anti-CD4 antibody
24	530.5	70.9	134	1 R54049	Sequence of the VH
25	530.5	70.9	134	1 W01526	Monoclonal antibody
26	530.5	70.9	134	1 W24986	Monoclonal antibody
27	529.5	70.8	121	1 R12270	Anti-human RHD FOM
28	529.5	70.8	476	1 W01818	Primate anti-CD4 he
29	529.5	70.8	476	1 W63761	Macaque primatized
30	527	70.5	118	1 R66329	Human immunoglobulin
31	527	70.5	125	1 P81259	Variable region of
32	526.5	70.4	139	1 W57446	Anti-CD4 antibody
33	521	69.7	118	1 R66322	Human immunoglobulin

34	515.5	68.9	528	1 R52952	Human anti-IgE Mab
35	514	68.7	120	1 R66343	Human immunoglobulin
36	508	67.9	119	1 R54799	SPA-reactive IgM h
37	507	67.8	107	1 R12287	Anti-human Rhd MAD
38	501	67.0	244	1 Y06718	Antibody 12E10 sin
39	499.5	66.8	117	1 R66320	Human immunoglobulin
40	495.5	66.2	119	1 W27554	Human Ab heavy cha
41	494	66.0	124	1 R12268	Anti-human Rhd FOG
42	493.5	66.0	117	1 R38659	Ab26. DNA segments
43	484	64.7	97	1 P50100	Sequence encoded b
44	476	63.6	124	1 W06474	Human lung cancer
45	471	63.0	116	1 R38670	268-D. DNA segment

ALIGNMENTS

RESULT	1	
ID	R66324	
AC	R66324	standard; Protein: 116 AA.
DT	03-AUG-1995	(first entry)
DE	Human immunoglobulin variable heavy chain #30.	
KW	primer; PCR; amplifi; human; immunoglobulin; variable; heavy chain;	
KV	cosmid; placenta; vector; pJB81; E.coli; mammalian.	
OS	Homo sapiens.	
PN	W09426895-A.	
PP	24-NOV-1984.	
RF	10-MAY-1993; J00603.	
PR	(N1SB) JAPAN TOBACCO INC.	
PI	Honjo T, Matsuda F;	
DR	WPI: 95-006791/01.	
DR	N-PDB: 078972.	
PT	DNA fragment comprising human immunoglobulin Vh genes - for the	
PS	production of human immunoglobulin in mammalian hosts	
PS	Clam 41; Page 74-75; 130pp; Japanese.	
CC	Protein sequences (R66295-51) are novel human immunoglobulin heavy chain	
CC	sequences encoded by novel isolated genes. The genes (078939-79002) were	
CC	isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21;	
CC	Y61Y24; 3-31; M84; M18 and M31, by PCR amplification using primers	
CC	Y618Y17-38. The genes are subdivided into 5 families of Vh genes. The	
CC	fragments cover a region of 800 kb. The DNA fragments were isolated from	
CC	high molecular weight DNA from human placenta. The DNA was partially	
CC	digested with TaqI restriction enzyme. The fragments were separated by	
CC	gel electrophoresis and 35-45 kb fractions were collected. The fragments	
CC	were ligated with ClaI-digested cosmid vector pJB81. The ligation	
CC	products were in vitro packaged and infected into E.coli 490A. The	
CC	fragments were then subcloned by colony hybridisation. The Vh genes and	
CC	the DNA fragments encoding them are useful in producing human	
CC	immunoglobulin in mammalian hosts.	
SQ	Sequence 116 AA;	

Query Match	83.2%; Score 622; DB 1; Length 116;
Best Local Similarity	100.0%; Pred. No. 3.8e-45;
Matches 116; Conservative	0; Mismatches 0; Indels 0; Gaps 0

QY	1	MKHLWFFLLVLAAPRWVLSQVQLQDGMGAGLSPSTLSLTCAVYGSGFSGYWMIRPP 60
DB	1	MKHLWFFLLVLAAPRWVLSQVQLQDGMGAGLSPSTLSLTCAVYGSGFSGYWMIRPP 60
QY	61	GKGLMEIENHSGSTNPNPSIKSRVTISVDTSKNQSFILKSSVTADTAVYYCAR 116
DB	61	GKGLMEIENHSGSTNPNPSIKSRVTISVDTSKNQSFILKSSVTADTAVYYCAR 116

RESULT	2	
ID	R93166	
AC	R93166	standard; Protein: 472 AA.
DT	30-OCT-1996	(first entry)
DE	Anti-Triehus D recombinant antibody D7C2 heavy chain.	

KM Human monoclonal antibody; immunoglobulin isotype IgM; agglutination;
 KW rhesus positive; rhesus negative; haemolysis; gamma 1 heavy chain;
 OS variable region; insect host cell; baculovirus; recombinant production.
 OS Homo sapiens.
 OS Synthetic.
 FT Key
 FT peptide
 FT 1.19
 FT /label="signal_peptide
 FT /note="mouse VH signal peptide sequence encoded by
 FT synthetic linker"
 FT 20.472
 FT protein
 FT /label="heavy chain
 FT /note="human gamma 1 chain constant region
 FT and the variable region from anti-rhesus D
 FT antibody D7C2"
 FT FR2724182-A1.
 PD 08-MAR-1996.
 PD 02-SEP-1994; FR-010566.
 PE 02-SEP-1994; FR-010566.
 (INSP) INST PASTEUR.
 PA (PROT-) PROTEINE PERFORMANCE.
 PI Chaabih H, Edelman L, Kaczorek M, Margartite C;
 DR WPI; 96-162018/17.
 DR N-PSDB; 726889.
 PT Recombinant anti-rhesus D monoclonal antibody - expressed by
 PT baculovirus-transformed insect cells and useful for preventing
 PT haemolysis in new-born babies
 PS Example 2; Page 35-37; 46pp; French.
 CC The human monoclonal antibody D7C2, of isotype IgM, recognises a
 CC 30-32 kD polypeptide on the membrane of rhesus positive red blood
 CC cells. The antibody agglutinates rhesus positive cells but not
 CC rhesus negative cells and is useful diagnostically and also for
 CC preventing haemolysis in new-born rhesus positive babies.
 CC Recombinant IgM-D7C2 can be produced by insect cells which have
 CC been transformed by a baculoviral vector comprising a D7C2
 CC expression cassette. The present sequence is that of a recombinant
 CC IgM-D7C2 heavy chain fused downstream of a mouse VH signal peptide.
 SO Sequence 472 AA;

Query Match 76.98; Score 575.5; DB 1; Length 472;

Best Local Similarity 85.28; Pred. No. 1.1e-40;

Matches 115; Conservative 3; Mismatches 14; Indels 3; Gaps 2;

QY 8 LLLAAPRWVLSOYVLOQMGAGLKPSETSLTCAVYGGSGYWMIRPPKGLWMI 67
 D 8 LFLVATGTVHSGVQVLOQMGAGLKPSETSLTCTVYGGSGYWMIRPPKGLWMI 67
 QY 68 GEINHSSTNNPILSKSRVTISVDTSKNQFSLKLSVTADTAAYYCAR--EIAAPH-R 124
 DB 68 GEINHSSTNNPILSKSRVTISVDTSKNQFSLKLSVTADTAAYYCARAEYKMKYNGD 127
 QY 125 YEDYWGQGLTVTVSS 139
 DB 128 WFDPMGQGTIVTVSS 142

RESULT 3

W24536
 ID W24536 standard; Protein; 136 AA.

AC W24536;

DT 09-OCT-1997 (first entry)

DE Immunoglobulin rB687 heavy chain variable region.

KW Immunoglobulin; variable region; heavy chain; thyrotropin receptor;

KM thyrotropin stimulating activity; light chain; Basedow's disease; antibody;

KW peripheral blood lymphocyte.

OS Homo sapiens.

FT Key
 FT peptide
 FT 1.19
 FT /note="signal peptide"

FT protein
 PN J09140386-A.
 PD 03-JUN-1997.

PE 22-NOV-1995; 328235.
 PR 22-NOV-1995; JP-328235.
 PA (EIKE) EIKEN KAGAKU KK.
 DR WPI; 97-344899/32.
 DR N-PSDB; 779919.
 PT Antibody containing immunoglobulin heavy chain mutation - with
 PT thyroid function stimulating activity
 PS Claim 31; Page 14-15; 18pp; Japanese.
 CC W24536-W24539 represent the immunoglobulin heavy and light chain variable
 CC regions isolated from peripheral blood lymphocyte strains. These
 CC sequences were isolated from the B687 and 101-2 strains of peripheral
 CC blood lymphocytes of a Basedow's disease patient. These sequences are
 CC replaced, deleted or inserted into an antibody, to create the antibodies
 CC of the invention. The antibodies of the invention have thyroid function
 CC stimulating activity, and act by combining with thyrotropin receptor. The
 CC antibody can be used in a method to detect autoantibodies which have
 CC thyroid function stimulating activity.
 SO Sequence 136 AA;

Query Match 74.98; Score 560.5; DB 1; Length 136;

Best Local Similarity 81.68; Pred. No. 5.7e-40;

Matches 111; Conservative 4; Mismatches 18; Indels 3; Gaps 2;

QY 1 MKHLMFLLVAPRWVLSOYVLOQMGAGLKPSETSLTCAVYGGSGYWMIRPP 60
 DB 1 MKHLMFLLVAPRWVLSOYVLOQMGAGLKPSETSLTCTVSGDSSITYSWIRPP 60
 QY 61 GKGLEWIGEINHSSTNNPILSKSRVTISVDTSKNQFSLKLSVTADTAAYYCAR-- 118
 DB 61 GKGLEWIGEINHSSTNNPILSKSRVTISVDTSKNQFSLKLSVTADTAAYYCARBERG 120
 QY 119 AARPHRY-FDYWGQGT 133
 DB 121 GLRDFAYGMDWGQGT 136

RESULT 4

W03757
 ID W03757 standard; Protein; 123 AA.

AC W03757;

DT 29-OCT-1996 (first entry)

DE Anti-rhesus D monoclonal antibody D7C2 heavy chain V region.

KW Human monoclonal antibody; immunoglobulin isotype IgM; agglutination;

KM rhesus positive; rhesus negative; haemolysis; heavy chain;

KW variable region; insect host cell; baculovirus; recombinant production.
 OS Homo sapiens.

FT Key
 FT region
 FT 29.35
 FT /label="CDR1
 FT /note="complementarity determining region"

FT region
 FT 50.65
 FT /label="CDR2
 FT /note="complementarity determining region"

FT region
 FT 98.112
 FT /label="CDR3
 FT /note="complementarity determining region"

FR2724182-A1.

PD 08-MAR-1996.

PE 02-SEP-1994; FR-010566.

PA (INSP) INST PASTEUR.

PA (PROT-) PROTEINE PERFORMANCE.

PI Chaabih H, Edelman L, Kaczorek M, Margartite C;

DR WPI; 96-162018/17.

DR N-PSDB; 726870.

PT Recombinant anti-rhesus D monoclonal antibody - expressed by

PT baculovirus-transformed insect cells and useful for preventing

PS haemolysis in new-born babies

PS Example 1; Page 32; 46pp; French.

CC The human monoclonal antibody D7C2, of isotype IgM, recognises a

CC 30-32 kD polypeptide on the membrane of rhesus positive red blood

CC cells. The antibody agglutinates rhesus positive cells but not

CC rhesus negative cells and is useful diagnostically and also for
 CC preventing haemolysis in new-born rhesus positive babies.
 CC Recombinant IGM-D7C2 can be produced by insect cells which have
 CC been transformed by a baculoviral vector comprising a D7C2
 CC expression cassette. The present sequence is that of the variable
 CC region of the IGM-D7C2 heavy chain.
 SQ Sequence 123 AA;

Query Match 74.7%; Score 558.5; DB 1; Length 123;
 Best Local Similarity 88.6%; Pred. No. 7.5e-40;
 Matches 109; Conservative 3; Mismatches 8; Indels 3; Gaps 2;

OY 20 QVQLQWAGALLKPKSESLTLCAYVGGSGFYWMIRPGKLENGEINHSSTNYN 79
 |||||
 DB 1 QVQLQWAGALLKPKSESLTLCAYVGGSGFYWMIRPGKLENGEINHSSTNYN 60
 |||||
 OY 80 PSLKSRVTISVDTSKNPSLTSLSSVTADTAIVYCAR--ELARPH-RYPDYWGGLT 136
 |||||
 DB 61 PSLKSRVTISVDTSKNPSLTSLSSVTADTAIVYCARARPEKMKYHGDWDPWGQGTIVT 120
 |||||
 OY 137 VSS 139
 |||||
 DB 121 VSS 123

RESULT 5

ID R41285
 AC R41285 standard; Protein; 142 AA.
 DT 01-NOV-1993 (first entry)
 DE F105 rearranged variable region heavy chain.
 KW Monoclonal antibody; Mab; envelope; glycoprotein; gp120; HIV; AIDS;
 KM CD4; receptor; hydridoma; polymerase chain reaction; PCR; heavy; light;
 KW chain; epitope; immune deficiency.
 OS Homo sapiens.
 FT key Location/Qualifiers
 FT peptide 1..19
 FT protein /label= sig-peptide
 FT protein /label= mat.protein
 PN NC0312232-A.
 PD 24-JUN-1993.
 PF 10-DEC-1992; U10928.
 PR 10-DEC-1991; US-804652.
 PA (DAND) DANA FARBER CANCER INST INC.
 PA (NEWME-) NEW ENGLAND DECONNESS HOSPITAL CORP.
 PA Haseltine WA, Marasco WA, Posner MR, Sodroski JG;
 H MPI: 93-214174/26.
 DB N-PSDB: 049154.
 PT DNA segments encoding monoclonal antibody - which binds to gp120
 PT and neutralises HIV, for treating AIDS, and for diagnosing and
 PT monitoring HIV infection
 PS Claim 9-10; Page 77; 109pp; English.
 CC mRNA from the known hydridoma F105 was converted to cDNA and this
 CC subjected to PCR amplification using primers corresp. to appropriate
 CC parts of the heavy or light chains and having restriction sites to
 CC permit cloning. The extension prods. were isolated and sequenced.
 CC The recombinant human monoclonal antibody (Mab) binds to a
 CC discontinuous epitope on the HIV gp120 envelope glycoprotein, blocks
 CC the binding of gp120 to the CD4 receptor, and neutralises a broad
 CC range of HIV isolates. The Mab may be used to treat immune
 CC deficiency, esp. at doses of 0.1-10 mg/kg.
 SQ Sequence 142 AA;

Query Match 74.7%; Score 558.5; DB 1; Length 142;
 Best Local Similarity 77.6%; Pred. No. 8.7e-40;
 Matches 111; Conservative 10; Mismatches 17; Indels 5; Gaps 2;

OY 1 MKHLMFLLVAADRWLSQVQLQWAGALLKPKSESLTLCAYVGGSGFYWMIRPG 60
 |||||
 DB 1 MEHLMFLLVAADRWLSQVQLQWAGALLKPKSESLTLCAYVGGSGFYWMIRPG 60
 |||||

OY 61 GKGLEWIGENHSSTNYNPSLKSRVTISVDTSKNPSLTSLSSVTADTAIVYCAR 120
 |||||
 DB 61 GKGLEWIGIYISGISTNYSLSKSRVTISVDTSKNPSLTSLSSVTADTAIVYCAR 120
 |||||
 OY 121 RPHRYFDY---WGQGLTYVSS 139
 |||||
 DB 121 AVF-YGDYRLDPMWGQGLTYVSS 142

RESULT 6

ID R12269
 AC R12269 standard; Protein; 128 AA.
 DT 15-AUG-1991 (first entry)
 DE Anti-human Rhd FOM-1 Mab (VH chain).
 KW Monoclonal antibody; rhesus D; blood-typing; CDR;
 KM hemolytic disease of the newborn; HDN.
 OS Homo sapiens.
 FT key Location/Qualifiers
 FT region 31..35
 FT region /label= CDR1
 FT region 50..65
 FT region /label= CDR2
 FT region 98..117
 FT region /label= CDR3
 PN NC0107492-A.
 PD 30-MAY-1991.
 PF 13-NOV-1990; E01964.
 PR 13-NOV-1989; GB-025590.
 PA (BLOO-) CENT BLOOD LAB AUTH.
 PI Hughes-Jones N;
 DR WPI: 91-178104/24.
 DR N-PSDB: Q11951.
 PT DNA encoding complementary determining regions - of human
 PT anti-rhesus D antibodies, useful in prodn. of monoclonal
 PT antibodies and for passive immunisation
 PS Disclosure; Fig 8: 32pp; English.
 CC The DNA sequence of eleven monoclonal antibodies are
 CC represented in Q119145-57. Synthetic genes, for both heavy and
 CC light chains may be created by combining selected CDR 1, 2, and 3
 CC regions, which may be selected from different antibody mole. having
 CC varied binding specificity. The chimeric anti-rhd antibodies can be
 CC used for diagnosis and therapy, and are capable of providing blood-
 CC typing reagents of high specificity and reliability. They can also
 CC be used in passive immunisation to prevent haemolytic disease of the
 CC newborn.
 SQ Sequence 128 AA;

Query Match 73.8%; Score 552; DB 1; Length 128;
 Best Local Similarity 83.7%; Pred. No. 2.7e-39;
 Matches 108; Conservative 4; Mismatches 7; Indels 10; Gaps 2;

OY 20 QVQLQWAGALLKPKSESLTLCAYVGGSGFYWMIRPGKLENGEINHSSTNYN 79
 |||||
 DB 1 QVQLQWAGALLKPKSESLTLCAYVGGSGFYWMIRPGKLENGEINHSSTNYN 60
 |||||
 OY 80 PSLKSRVTISVDTSKNPSLTSLSSVTADTAIVYCARIELARPHR-----YFDYWG 130
 |||||
 DB 61 PSLKSRVTISVDTSKNPSLTSLSSVTADTAIVYCARGL-ERIRNDQLNRLGYMDWVG 119
 |||||
 OY 131 QGLTYVSS 139
 |||||
 DB 120 KGLTYVSS 128

RESULT 7
 ID R42689
 AC R42689 standard; Protein; 116 AA.
 DT 01-NOV-1993 (first entry)
 DE Vh 71-A*

CC Y6.Y24;3-31; M84; M18 and M31, by PCR amplification using primers
CC Q89917-38. The genes are subdivided into 5 families of Vh genes. The
CC fragments cover a region of 800 kb. The DNA fragments were isolated from
CC high molecular weight DNA from human placenta. The DNA was partially
CC digested with *Hpa*I restriction enzyme. The fragments were separated by
CC gel electrophoresis and 35-45 kb fractions were collected. The fragments
CC were ligated with *Cla*I-digested cosmid vector pJ81. The ligation
CC products were in vitro packed and infected into E.coli 490A. The
CC fragments were then subcloned by colony hybridisation. The Vh genes and
CC the DNA fragments encoding them are useful in producing human
SC immunoglobulin in mammalian hosts.

SQ Sequence 116 AA;

Query Match 73.5%; Score 550; DB 1; Length 116;
Best Local Similarity 90.5%; Pred. No. 3,6e-39;
Matches 105; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 MKHLMEFLLVAAPRWVLSOVOLQMGAGLKPSETSLTCAVYGSGFYWMIROP 60
DB 1 MKHLMEFLLVAAPRWVLSOVOLQESGGLVPKSETSLTCTVCSGSVSYYWMIRPP 60
||||| : ||||| : ||||| : ||||| : ||||| :
OY 61 GKGLEWIEINHSSTNPNPLSKSVTTSVPTSKNOFSIKLSSVTAAATPANYCYAR 116
DB 61 GKGLEWIDITYSSTNPSPKSKSVTTSVPTSKNOFSIKLSSVTAAATPANYCYAR 116
||||| : ||||| : ||||| : ||||| : ||||| :
RESULT 9
ID W01822 standard; Protein; 476 AA.
AC W01822:
DT 25-MAY-1997 (first entry)
DE Primatised anti-human B7.1 antigen antibody 16C10 heavy chain.
KW Monoclonal antibody; cynomolgus monkey; macaque; 16C10;
KV Primatised antibody; B7 antigen; CD28; immunosuppressive;
KW autoimmune disease; idiopathic thrombocytopaenia purpura;
systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KM type 1 diabetes mellitus; graft versus host disease;
KW hetero-hybridoma; transfectoma.
OS Chimeric Macaca cynomolgus;
OS Chimeric Homo sapiens.
PN W09640878-A1.
PD 19-DEC-1996.
PE 06-JUN-1996; U10053.
PR 07-JUN-1995; US-487350.
PI (IDEC-) IDEC PHARM CORP.
PI Anderson DR, Brams P, Hanna N, Slesowsky WS;
DR WPI; 97-108638/10.
PI N-PSDB; T62513.
PT Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PS useful for treating autoimmune disease or graft-versus-host disease
PS Claim 14; Fig 10B; 81pp; English.
PZ 2 polypeptides (W01821 and W01822) respectively comprise primatised
CC forms of the light and heavy chains of cynomolgus monkey anti-human
CC B7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and
CC heavy variable genes (see also T62512 and T62513) are inserted into
CC an expression vector (pref. MCS2RA) which contains human light and
CC heavy chain constant region genes to allow prodn. Of the primatised
CC antibody in e.g. CHO cells. Primatised 7C10 and 7B6 anti-B7.1
CC antibodies have also been produced (see also W01817-20). The
CC primatised antibodies inhibit the B7/CD28 pathway, making them
CC useful immunosuppressants for the treatment of autoimmune disorders
CC and graft-versus-host disease.

SQ Sequence 476 AA;

Query Match 72.4%; Score 541.5; DB 1; Length 476;
Best Local Similarity 74.0%; Pred. No. 7.7e-38;
Matches 108; Conservative 11; Mismatches 20; Indels 7; Gaps 3;

OY 1 MKHLMFLLVAAPRWVLSOVOLQMGAGLKPSETSLTCAVYGSGFS-GIYWSMIRPP 59
DB 1 MKHLMFLLVAAPRWVLSOVOLQESGGLVPKSETSLTCAVSGSISGGYGMCMIRPP 60
||||| : ||||| : ||||| : ||||| : ||||| :
||||| : ||||| : ||||| : ||||| : ||||| :

PT produced by primer amplification, used in the diagnosis of HCMV
 PT Infection
 CC Claim 4: Page 16-18: 22pp; Japanese.
 CC The sequences given in R63553-54 represent the heavy and light chains
 CC respectively of a monoclonal antibody against a 65 kD antigen of human
 CC cytomegalovirus (HCMV). The DNA's encoding these sequences were
 CC amplified using the sequences given in T18040-58. The monoclonal
 CC antibody may be used in the diagnosis of HCMV.
 SQ Sequence 475 AA;

Query Match 72.1%; Score 539; DB 1; Length 475;
 Best Local Similarity 74.5%; Pred. No. 1.2e-37;
 Matches 111; Conservative 6; Mismatches 18; Indels 14; Gaps 3;

OY 1 MKHMFLLVAPRWLSQVLOQMGAGLKPSETSLTCAYVGGSGF--SGYWSMIRQ 58
 ||||||| :
 DB 1 MKHMFLLVAPRWLSQVLOQMGAGLKPSETSLTCAYVGGSGF--SGYWSMIRQ 60
 59 PGKGLMEIGINHSSTYNPNSLSKRYTISVDTSKNOFSLKLSVTADTAAYTCAREI 118
 ||||||| :
 DB 61 PGKGLMEIGITGSGTINPNSLSKRYTISVDASNNQFSLKLSVTADTAAYTCAR-- 118
 ||||||| :
 OY 119 AARPHRYFD-----YMGGLTVTVSS 139
 :
 DB 119 -TSPQYDILTGSGFSPYWGGLTVTVSS 145

RESULT 13
 ID R66298 standard; Protein; 116 AA.
 AC R66298;
 DT 07-AUG-1995 (first entry)
 DE Human immunoglobulin variable heavy chain #4.
 KM Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain;
 KW cosmid; placenta; vector; pJB81; E.coli; mammalian.
 OS Homo sapiens.
 PN M09426895-A.
 PD 24-NOV-1994.
 PF 10-MAY-1993; J00603.
 PR 10-MAY-1993; NO-J00603.
 PA (NIBS) JAPAN TOBACCO INC.
 PI Honjo T, Matsuda F;
 DR N-PSDB; 078942.
 PT DNA fragment comprising human immunoglobulin Vh genes - for the
 PT production of human immunoglobulin in mammalian hosts
 P1 disclosure: Page 34-35; 130pp; Japanese.
 CC Protein sequences (R66295-51) are novel human immunoglobulin heavy chain
 CC sequences encoded by novel isolated genes. The genes (078939-79002) were
 CC isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21;
 CC Y6; Y24; 3-31; M84; M118 and M131, by PCR amplification using primers
 CC 078917-38. The genes are subdivided into 5 families of Vh genes. The
 CC fragments cover a region of 800 kb. The DNA fragments were isolated from
 CC high molecular weight DNA from human placenta. The DNA was partially
 CC digested with Taqi restriction enzyme. The fragments were separated by
 CC gel electrophoresis and 35-45 kb fractions were collected. The fragments
 CC products were ligated with ClaI-digested cosmid vector pJB81. The ligation
 CC fragments were then subcloned and infected into E.coli 490A. The
 CC the DNA fragments encoding them are useful in producing human
 CC immunoglobulin in mammalian hosts.
 SQ Sequence 116 AA;

Query Match 71.9%; Score 538; DB 1; Length 116;
 Best Local Similarity 88.8%; Pred. No. 3.5e-38;
 Matches 103; Conservative 3; Mismatches 10; Indels 0; Gaps 0;
 OY 1 MKHMFLLVAPRWLSQVLOQMGAGLKPSETSLTCAYVGGSGFSGSYWSMIRQ 60
 ||||||| :
 DB 1 MKHMFLLVAPRWLSQVLOQMGAGLKPSETSLTCAYVGGSGFSGSYWSMIRQ 60

OY 61 GKGLMEIGINHSSTYNPNSLSKRYTISVDTSKNOFSLKLSVTADTAAYTCAR 116
 ||||||| :
 DB 61 GKGLMEIGITGSGTINPNSLSKRYTISVDASNNQFSLKLSVTADTAAYTCAR 118

RESULT 14
 ID W32477 standard; Protein; 140 AA.
 AC W32477;
 DT 16-JAN-1998 (first entry)
 DE Anti-CD4 cytomoligus monkey immunoglobulin heavy chain variable region.
 KM Anti-CD4 antibody; cytomoligus monkey; immunoglobulin; Ig;
 KW chimpanzee; chimeric antibody; human therapy; Old World monkey;
 OS macaca fascicularis.
 PN US5658570-A.
 PD 19-AUG-1997.
 PF 25-JUL-1991; 735064.
 PR 10-JUL-1992; US-912292.
 PR 25-JUL-1991; US-735064.
 PR 23-MAR-1992; US-856281.
 PR 25-JAN-1993; US-379072.
 PA (IDEC-) IDEC PHARM CORP.
 PI Hanna N, Newman RA, Raab RW;
 DR N-PSDB; T91564.
 PT Chimeric antibodies for human therapy - comprising human or
 PT chimpanzee immunoglobulin constant region and an Old World monkey
 PT antigen-binding region
 PS Example 3; Fig 13; 46pp; English.
 CC A new chimeric antibody (Ab) has been developed comprising a human or
 CC chimpanzee immunoglobulin (Ig) constant region and an Old World monkey
 CC antigen (Ag)-binding region. The present sequence represents an anti-CD4
 CC cynomolgus monkey Ig heavy chain variable region. An anti-CD4 antibody
 CC (Ab) comprising the light- and heavy-chain variable regions encoded by
 CC DNA corresponding to the light- and heavy-chain variable regions of Old
 CC new. The Abs are useful for human therapy, especially of tumors. Old
 CC world monkeys are sufficiently different from humans to allow Abs
 CC against human Ags, even relatively conserved Ags such as CD4 and CD54,
 CC to be raised in these monkeys, and are sufficiently similar to humans to
 CC avoid host anti-Ab immune responses when the Abs are introduced into
 CC humans.
 SQ Sequence 140 AA;

Query Match 71.7%; Score 536.5; DB 1; Length 140;
 Best Local Similarity 77.3%; Pred. No. 5.7e-38;
 Matches 109; Conservative 7; Mismatches 22; Indels 3; Gaps 3;

OY 1 MKHMFLLVAPRWLSQVLOQMGAGLKPSETSLTCAYVGGSGFSG--YWSMIRQ 59
 ||||||| :
 DB 1 MKHMFLLVAPRWLSQVLOQMGAGLKPSETSLTCAYVGGSGFSG--YWSMIRQ 60
 60 PGKGLMEIGINHS--GSTYNPNSLSKRYTISVDTSKNOFSLKLSVTADTAAYTCAREI 118
 ||||||| :
 DB 61 PGKGLMEIGITGSGTINPNSLSKRYTISVDASNNQFSLKLSVTADTAAYTCASNI 120
 ||||||| :
 OY 119 AARPHRYFDWGGGLTVTVSS 139
 :
 DB 121 LKYLH-WLLYWGGLTVTVSS 140

RESULT 15
 ID W43430 standard; Protein; 140 AA.
 AC W43430;
 DT 05-MAY-1998 (first entry)
 DE Monkey anti-CD4 heavy chain variable region protein sequence.
 KM Primer; PCR; amplification; leader sequence; human; monkey; baboon;
 KW macaque; immunoglobulin; heavy chain variable region; chimpanzee; hybrid;
 KW lymphoma; AIDS; autoimmune disease; inflammatory disease; transplant;
 OS macaca cynomolgus.
 SQ Sequence 140 AA;

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Int. Immunol. 3, 865-875, 1991
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and high-affinity B cell receptors.
A:Reference number: S23716; MUID:92031262
A:Accession: S23717

A:Molecule type: mRNA
A:Residues: 15-111 <HAW>
A:Cross-references: EMBL:X54441
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: Immunoglobulin
F:1-14/Domain: signal sequence (fragment) #status predicted <SIG>
F:15-140/Product: Ig heavy chain (fragment) #status predicted <HAW>
F:29-111/Domain: Immunoglobulin homology <IMM>

Query Match 85.7%; Score 641; DB 2; Length 140;
Best Local Similarity 88.7%; Pred. No. 7.9e-51;
Matches 126; Conservative 1; Mismatches 5; Indels 10; Gaps 2;

0 6 FELLVAAPRWLSQVQLQDGMGAGLKPSETLSLTCAVYGGSGFYWSWIRPGKLE 65
1 FELLVAAPRWLSQVQLQDGMGAGLKPSETLSLTCAVYGGSGFYWSWIRPGKLE 60
Db 1 FELLVAAPRWLSQVQLQDGMGAGLKPSETLSLTCAVYGGSGFYWSWIRPGKLE 60
Qy 66 WIGELINHSSTNPNPSLKSRYTISVDTSKNPSLKLSTVTAADTAAYTCAR-----E 117
Db 61 WIGELINHSSTNPNPSLKSRYTISVDTSKNPSLKLSTVTAADTAAYTCARSGSLGLE 120
Qy 118 IAPRHFEDYWGQGLTVYSS 139
Db 121 WLPF--AFDYWGQGLTVYSS 140

RESULT 3
13782
Ig variable region (VDJ) (clone T23-9) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-1999
C:Accession: J3782; S25476
R:Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A:Title: Somatic diversification in the heavy chain variable region genes expressed by B cells.
A:Reference number: A36876; MUID:94119917
A:Accession: J3782
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-140 <RES>
A:Cross-references: EMBL:X67906; NID:933582; PDB:CAA48104.1; PID:933583
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
F:28/Domain: Immunoglobulin homology <IMM>

Query Match 83.6%; Score 625.5; DB 2; Length 140;
Best Local Similarity 86.4%; Pred. No. 2e-49;
Matches 121; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

Qy 1 MKHLMFELLVAAPRWLSQVQLQDGMGAGLKPSETLSLTCAVYGGSGFYWSWIRPP 60
Db 1 MKHLMFELLVAAPRWLSQVQLQDGMGAGLKPSETLSLTCTVSGGSISFYWSWIRPP 60
Qy 61 GKGLEWIGTINHSSTNPNPSLKSRYTISVDTSKNPSLKLSTVTAADTAAYTCARETAA 120
Db 61 GKGLEWIGTINHSSTNPNPSLKSRYTISVDTSKNPSLKLSTVTAADTAAYTCARETAA 120
Qy 121 RPH-RYEDYWGQGLTVYSS 139
Db 121 SWYGRFYEDYWGQGLTVYSS 140

RESULT 4
S31586
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S31586
R:Cushtier, A.M.; Gauthier, L.; Boudil, L.; Fougereau, M.; Tonnelle, C.
Submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from t

A:Reference number: S31585
A:Accession: S31586
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-139 <CTI>
A:Cross-references: EMBL:Z14182; NID:930978; PDB:CAA78551.1; PID:930979
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:34-116/Domain: Immunoglobulin homology <IMM>

Query Match 78.7%; Score 589; DB 2; Length 139;
Best Local Similarity 82.7%; Pred. No. 3.7e-46;
Matches 115; Conservative 4; Mismatches 20; Indels 0; Gaps 0;

Qy 1 MKHLMFELLVAAPRWLSQVQLQDGMGAGLKPSETLSLTCAVYGGSGFYWSWIRPP 60
Db 1 MKHLMFELLVAAPRWLSQVQLQDGMGAGLKPSETLSLTCTVSGGSISFYWSWIRPPA 60
Qy 61 GKGLEWIGTINHSSTNPNPSLKSRYTISVDTSKNPSLKLSTVTAADTAAYTCARETAA 120
Db 61 GKGLEWIGTINHSSTNPNPSLKSRYTISVDTSKNPSLKLSTVTAADTAAYTCARETAA 120
Qy 121 RPHRYEDYWGQGLTVYSS 139
Db 121 IRGAFIDYWGQGLTVYSS 139

RESULT 5
S31676
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31676
R:Cushtier, A.M.; Gauthier, L.; Boudil, L.; Fougereau, M.; Tonnelle, C.
Submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from t
A:Reference number: S31676
A:Accession: S31676
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-137 <CTI>
A:Cross-references: EMBL:Z14182; NID:931031; PDB:CAA78551.1; PID:931032
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:34-116/Domain: Immunoglobulin homology <IMM>

Query Match 78.2%; Score 585; DB 2; Length 137;
Best Local Similarity 82.9%; Pred. No. 8.3e-46;
Matches 116; Conservative 4; Mismatches 16; Indels 4; Gaps 2;

Qy 1 MKHLMFELLVAAPRWLSQVQLQDGMGAGLKPSETLSLTCAVYGGSGFYWSWIRPP 60
Db 1 MKHLMFELLVAAPRWLSQVQLQDGMGAGLKPSETLSLTCTVSGGSISFYWSWIRPPA 60
Qy 61 GKGLEWIGTINHSSTNPNPSLKSRYTISVDTSKNPSLKLSTVTAADTAAYTCARETAA 120
Db 61 GKGLEWIGTINHSSTNPNPSLKSRYTISVDTSKNPSLKLSTVTAADTAAYTCARETAA 120
Qy 121 RPHRYEDYWGQGLTVYSS 139
Db 118 APLMYGMDYWGQGLTVYSS 137

RESULT 6
S13519
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)

C:Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S13519
R:Moritani, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.M.
Nucleic Acids Res. 19, 673, 1991
A:Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked
A:Reference number: S13519; MUID:9118791
A:Accession: S13519
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-147 <MOR>
A:Cross-references: EMBL:X56158; NID:q37724; PIDN:CAA3626.1; PID:q37725
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:41-125/Domain: Immunoglobulin homology <IM>

Query Match 78.1%; Score 584.5; DB 2; Length 147;
Best Local Similarity 82.3%; Pred. No. 9.9e-46;
Matches 116; Conservative 5; Mismatches 17; Indels 3; Gaps 2;

1 MKHMFLLVAARWVLSQVQLQDQMGAGLKPSSETLSITCAVYGGSF--SGYYSWIRQ 58
|||||
8 MKHMFLLVAARWVLSQVQLQDQMGAGLKPSSETLSITCAVYGGSFSSSSSYWGWIRQ 67
|||||
59 PPGKLEWIGETINHGSGTNYNPSLKSRYTISVDTSKNQFSLKLSVTADTAVYVCAREI 118
|||||
68 PPGKLEWIGETINHGSGTNYNPSLKSRYTISVDTSKNQFSLKLSVTADTAVYVCAREI 127
|||||
119 AARPRYEDYWGQGLTVTVSS 139
|||||
128 LMF-GELEDYWGQGLTVTVSS 147
|||||

RESULT 7
Ig heavy chain precursor V-D-J region (clone mAb 67VH) - human (fragment)
S78055

C:Species: Homo sapiens (man)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78055; S23720
R:Harindranath, N.
Submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78055

A:Molecule type: mRNA
A:Residues: 1-145 <HAR>
A:Cross-references: EMBL:X54445; NID:q37817; PIDN:CAA38312.1; PID:q37818
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Immunol. 3, 865-875, 1991
A:Note: Complete sequence of the gene encoding the V(H) and V(L) regions of low- and h
patient.
A:Reference number: S23716; MUID:92031262

A:Accession: S23720
A:Molecule type: mRNA
A:Residues: 18-115 <HAW>
A:Cross-references: EMBL:X54445
A:Note: the authors translated the codon GCA for residue 67 as Arg
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: Immunoglobulin
F:1-17/Domain: signal sequence (fragment) #status predicted <SIG>
F:18-145/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:32-115/Domain: Immunoglobulin homology <IM>

Query Match 77.0%; Score 576; DB 2; Length 145;
Best Local Similarity 79.5%; Pred. No. 5.7e-45;
Matches 116; Conservative 6; Mismatches 14; Indels 10; Gaps 3;

3 HMFELLLVAARWVLSQVQLQDQMGAGLKPSSETLSITCAVYGGSF--SGYYSWIRQPPG 61
|||||
1 HMFELLLVAARWVLSQVQLQDQMGAGLKPSSETLSITCAVYGGSFSSSSSYWGWIRQPPG 60
|||||
62 KLEWIGETINHGSGTNYNPSLKSRYTISVDTSKNQFSLKLSVTADTAVYVCAREIA- 120
|||||

Db 61 KLEWIGETINHGSGTNYNPSLKSRYTISVDTSKNQFSLKLSVTADTAVYVCAREI 120
Oy 121 -----RPRYEDYWGQGLTVTVSS 139
|:|||||
Db 121 FWSGYTRGY-YFDYWGQGLTVTVSS 145
|:|||||

RESULT 8

Ig heavy chain precursor V-II region (ARH-77) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 02-Sep-1997
C:Accession: A02101
R:Kudo, A.; Ishihara, T.; Nishimura, Y.; Watanabe, T.
Gene 33, 181-189, 1985
A:Title: A cloned human immunoglobulin heavy chain gene with a novel direct-repeat se
A:Reference number: A02101; MUID:85205332
A:Accession: A02101

A:Molecule type: mRNA
A:Residues: 1-146 <KUD>

A:Note: the sequence was determined from the differentiated gene
A:Note: the authors translated the codon GGG for residue 17 as Arg
C:Genetics:

A:Gene: GDB:IGHV
A:Cross-references: GDB:128528; OMIM:147070
A:Map position: 14q32.33-14q32.33

A:Introns: 16/3
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-146/Product: Ig heavy chain V-II region (ARH-77) #status predicted <MAT>
F:20-117/Region: V segment
F:35-117/Domain: Immunoglobulin homology <IM>
F:118-127/Region: D segment
F:128-146/Region: J segment
F:42-115/Disulfide bonds: #status predicted

Query Match 76.4%; Score 571.5; DB 1; Length 146;
Best Local Similarity 78.1%; Pred. No. 1.5e-44;
Matches 114; Conservative 5; Mismatches 20; Indels 7; Gaps 2;

1 MKHMFLLVAARWVLSQVQLQDQMGAGLKPSSETLSITCAVYGGSFSGYYSWIRQ 59
|||||
1 MKHMFLLVWCQLPDVGLSQVQLQDQMGAGLKPSSETLSITCAVYGGSFSGYYSWIRQ 60
|||||

60 PPGKLEWIGETINHGSGTNYNPSLKSRYTISVDTSKNQFSLKLSVTADTAVYVCAREIA 119
|||||
61 PPGKLEWIGETINHGSGTNYNPSLKSRYTISVDTSKNQFSLKLSVTADTAVYVCAREIA 120
|||||

120 AARPRYEDY-----WGQGLTVTVSS 139
||
121 RGNWVDVYGGMDYWGQGLTVTVSS 146
|||||

RESULT 9

Ig heavy chain V4.21-UniqueD-J5 region - human
S47010
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S47010

R:Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
submitted to the EMBL Data Library, July 1994
A:Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody
A:Reference number: S47009
A:Accession: S47010

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-126 <MAH>

A:Cross-references: EMBL:Z35492; NID:q517254; PIDN:CAA84625.1; PID:q517255
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; Immunoglobulin
F:15-97/Domain: Immunoglobulin homology <IM>

Query Match 76.3%; Score 571; DB 2; Length 126;
Best Local Similarity 87.3%; Pred. No. 1.4e-44;

Matches 110; Conservative 3; Mismatches 7; Indels 6; Gaps 1;

OY 20 QVQLQMGAGLLPSETSLTCAVYGGSGYWSWIROPGRGLEWIGELINSGSTNTN 79
|||||

DB 1 QVQLQMGAGLLPSETSLTCAVYGGSGYWSWIROPGRGLEWIGELINSGSTNTN 60
|||||

OY 80 PSLKSVTISVDTSKNOFSLKSVTAADTAVYCCAR-----ETARRHRYFDYGGGT 133
|||||

DB 61 PSLKSVTISVDTSKNOFSLKSVTAADTAVYCCAR-----ETARRHRYFDYGGGT 120
|||||

OY 134 LVTVSS 139
|||||

DB 121 LVTVSS 126
|||||

RESULT 10
S31512
Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C:Accession: S31512

R:Chastagner, A.M.; Gauthier, L.; Boubil, L.; Fougereau, M.; Tonnelie, C.

submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585

A:Accession: S31586

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-139 <CD>

A:Cross-references: EMBL:Z14194; NID:930975; PIDN:CAA76563.1; PID:930976

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 76.3%; Score 570.5; DB 2; Length 139;
Best Local Similarity 81.5%; Pred. No. 1.7e-44;

Matches 110; Conservative 6; Mismatches 18; Indels 1; Gaps 1;

OY 1 MKHMFLLVAAPRWVLSQVQLQMGAGLLPSETSLTCAVYGGSGYWSWIROP 60
|||||

DB 1 MKHMFLLVAAPRWVLSQVQLQMGAGLLPSETSLTCAVYGGSGYWSWIROP 60
|||||

OY 61 GKGLWIGELINSGSTNTNPSLKSRTISVDTSKNOFSLKSVTAADTAVYCCAR-EIA 119
|||||

DB 61 AKGLEWIGRTTSGSTNTNPSLKSRTISVDTSKNOFSLKSVTAADTAVYCCARGGIG 120
|||||

OY 120 ARPHRYFDYGGGT 134
|||||

DB 121 LTGDKWDYWGQGT 135
|||||

RESULT 11
S31511
Ig heavy chain - human

C:Species: Homo sapiens (man)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S31511

R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.

submitted to the EMBL Data Library, December 1992

A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto

A:Reference number: S31509

A:Accession: S31511

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-155 <CH>

A:Cross-references: EMBL:X69866; NID:933094; PIDN:CAA49500.1; PID:933095

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:47-129/Domain: immunoglobulin homology <IMM>

Query Match 76.1%; Score 569.5; DB 2; Length 155;
Best Local Similarity 77.8%; Pred. No. 2.3e-44;

Matches 112; Conservative 7; Mismatches 18; Indels 7; Gaps 2;

OY 1 MKHMFLLVAAPRWVLSQVQLQMGAGLLPSETSLTCAVYGGSGYWSWIROP 60
|||||

DB 14 MKHMFLLVAAPRWVLSQVQLQMGAGLLPSETSLTCAVYGGSGYWSWIROP 73
|||||

OY 61 GKGLWIGELINSGSTNTNPSLKSRTISVDTSKNOFSLKSVTAADTAVYCCAR-ETAA 120
|||||

DB 74 GKGLWIGELINSGSTNTNPSLKSRTISVDTSKNOFSLKSVTAADTAVYCCAR--GG 131
|||||

OY 121 RPHRYDY----WGQGT 139
|||||

DB 132 GISSWYDYGGMDYWGQGT 155
|||||

RESULT 12
S31512
Ig heavy chain - human

C:Species: Homo sapiens (man)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S31512

R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.

submitted to the EMBL Data Library, December 1992

A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA a

A:Reference number: S31509

A:Accession: S31512

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-155 <CH>

A:Cross-references: EMBL:X69860; NID:933082; PIDN:CAA49494.1; PID:933083

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:47-129/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 563.5; DB 2; Length 155;
Best Local Similarity 78.9%; Pred. No. 8.1e-44;

Matches 112; Conservative 8; Mismatches 19; Indels 3; Gaps 2;

OY 1 MKHMFLLVAAPRWVLSQVQLQMGAGLLPSETSLTCAVYGGSGYWSWIROP 60
|||||

DB 14 MKHMFLLVAAPRWVLSQVQLQMGAGLLPSETSLTCAVYGGSGYWSWIROP 73
|||||

OY 61 GKGLWIGELINSGSTNTNPSLKSRTISVDTSKNOFSLKSVTAADTAVYCCAR--ET 118
|||||

DB 74 GKGLWIGELINSGSTNTNPSLKSRTISVDTSKNOFSLKSVTAADTAVYCCARGGI 133
|||||

OY 119 ARPHRY-FDYWGQGT 139
|||||

DB 134 SSWYDYGGMDYWGQGT 155
|||||

RESULT 13
S09711
Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996

C:Accession: S09711

R:Bughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.

Biochem. J. 268:135-140, 1990

A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domain

A:Reference number: S09710; MUID:9026235

A:Accession: S09711

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-146 <HD>

A:Cross-references: EMBL:X69866; NID:933094; PIDN:CAA49500.1; PID:933095

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

C;Keywords: heterotetramer; immunoglobulin F₁₅-97/Domain: immunoglobulin homology <IMM>

Job time: 3442 sec

C;Keywords: heterotetramer; immunoglobulin F₁₅-97/Domain: immunoglobulin homology <IMM>

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OM protein - protein search, using sw model

Run on: July 26, 2000, 14:03:14 ; Search time 12.18 Seconds

(without alignments)
353.652 Million cell updates/sec

Title: US-09-203-768a-2
Perfect score: 748

Sequence: 1 MKHLMEFLLVAPRWLSQ.....ARPHRYDYGCGTLVTSS 139

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 85661 seqs, 30989116 residues

To: number of hits satisfying chosen parameters: 85661

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SWISSProt_38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	571.5	76.4	146	1	P06331 homo sapien
2	411.5	55.0	129	1	P01824 homo sapien
3	408	54.5	137	1	P01822 mus musculu
4	397.5	53.1	117	1	P01825 homo sapien
5	370	49.5	116	1	P01831 mus musculu
6	369.5	49.4	144	1	P01819 mus musculu
7	359.5	48.1	113	1	P01823 mus musculu
8	359.5	48.1	135	1	P20957 xenopus lae
9	343	45.9	116	1	P01853 mus musculu
10	330	44.1	139	1	P01751 mus musculu
11	329	44.0	137	1	P01755 mus musculu
12	328	43.9	119	1	P01807 mus musculu
13	326.5	43.6	117	1	P01853 mus musculu
14	326	43.6	119	1	P01808 mus musculu
15	325	43.4	119	1	P01810 mus musculu
16	323.5	43.2	138	1	P03980 mus musculu
17	322	43.0	122	1	P01768 homo sapien
18	321	42.9	136	1	P20956 xenopus lae
19	317.5	42.4	117	1	P01811 mus musculu
20	316.5	42.3	118	1	P01809 mus musculu
21	316.5	42.3	142	1	P01805 rattus norv
22	315	42.2	115	1	P01820 mus musculu
23	310	41.4	120	1	P06329 mus musculu
24	306.5	41.0	123	1	P01791 mus musculu
25	305.5	40.8	121	1	P01745 mus musculu
26	304	40.6	116	1	P01821 mus musculu
27	303.5	40.6	115	1	P01765 homo sapien
28	303.5	40.6	117	1	P01812 mus musculu
29	302.5	40.4	117	1	P01757 mus musculu
30	302.5	40.4	140	1	P01746 mus musculu
31	300.5	40.2	117	1	P01756 mus musculu
32	300.5	40.2	121	1	P01771 homo sapien
33	299	40.0	147	1	P04438 homo sapien

34	297	39.7	120	1	HY2B_HUMAN	P01815 homo sapien
35	296	39.6	118	1	HY51_MOUSE	P06330 mus musculu
36	295.5	39.5	120	1	HY03_MOUSE	P01747 mus musculu
37	295.5	39.5	123	1	HY18_MOUSE	P01787 mus musculu
38	295.5	39.5	123	1	HY19_MOUSE	P01788 mus musculu
39	294.5	39.4	123	1	HY23_MOUSE	P01792 mus musculu
40	293	39.2	122	1	HY3H_HUMAN	P01769 homo sapien
41	292.5	39.1	119	1	HY2C_HUMAN	P01816 homo sapien
42	290.5	38.8	117	1	HY04_MOUSE	P01748 mus musculu
43	289.5	38.6	117	1	HY17_MOUSE	P01786 mus musculu
44	288	38.5	122	1	HY20_MOUSE	P01789 mus musculu
45	287.5	38.4	116	1	HY36_MOUSE	P01806 mus musculu

ALIGNMENTS

RESULT	ID	HY2I_HUMAN	STANDARD:	PRT:	146 AA.
AC	P06331:				
DR	01-JAN-1988 (Rel. 06, Created)				
DT	01-JAN-1988 (Rel. 06, Last sequence update)				
DE	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	IG HEAVY CHAIN V-II REGION ARH-77 PRECURSOR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 85205332.				
RA	Kudo A., Ishihara T., Nishimura Y., Watanabe T.;				
RT	"A Cloned human Immunoglobulin heavy chain gene with a novel direct-				
RL	repeat sequence in 5' flanking region."				
DR	Gene 33:181-189(1985).				
DR	PIR: A02101; G1HGH2.				
DR	HSSP: P01825; 7FAB.				
DR	PFAM: PF00047; 19; 1.				
KW	Immunoglobulin V region; Signal.				
FT	SIGNAL	1	19		
FT	CHAIN	20	146		IG HEAVY CHAIN V-II REGION ARH-77.
FT	DOMAIN	20	117		V SEGMENT.
FT	DOMAIN	118	127		D SEGMENT.
FT	DOMAIN	128	146		J SEGMENT.
FT	DISULFID	42	115		BY SIMILARITY.
FT	NON_TER	146	146		
SQ	SEQUENCE	146 AA;	16228 MW;	807FD52BB218171F	CRC64;
Query Match					
Best Local Similarity 76.4%; Score 571.5; DB 1; Length 146;					
Matches 114; Conservative 5; Mismatches 20; Indels 7; Gaps 2;					
QY	1	MKHLMEFLLVAPRWLSQVQLOQMGGLKPSSETSLTCAVYGGSSGYGWSMIRP	59		
DB	1	MKHLMEFLLVAPRWLSQVQLOQMGGLKPSSETSLTCAVYGGSSGYGWSMIRP	60		
QY	60	PKGLGEWIGEINHSSTNPNPSIKSRVTISVDTSKNOFSIKLSTYADTAVYICAREIA	119		
DB	61	PKGLGEWIGEINHSSTNPNPSIKSRVTISVDTSKNOFSIKLSTYADTAVYICAREIA	120		
QY	120	ARPHRYDYGCGTLVTSS	139		
DB	121	RGGMNDVYVYGGMDVWGCGTLVTSS	146		
RESULT 2					
ID	HY2F_HUMAN	STANDARD:	PRT:	129 AA.	
AC	P01824:				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				

DE IG HEAVY CHAIN V-II REGION WASH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 RN Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RP [1]
 RX SEQUENCE.
 RA MEDLINE: 82222235.
 RA Takahashi N., Tetaert D., Debaille B., Lin L.-C., Putnam F.W.;
 RT "Complete amino acid sequence of the delta heavy chain of human
 immunoglobulin D.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2850-2854(1982).
 CC -1 MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGD MYELOMA
 CC PROTEIN.
 DR PIR: A02099; D2HUMA.
 DR HSSP: P01825; 7FAB.
 DR PFAM: PF00047; 1g; 1.
 KW Immunoglobulin V region.
 FT NON_TER 129 129
 SS SEQUENCE 129 AA; 14117 MW; D5D3D47ABE51319 CRC64;
 Query Match 55.0%; Score 411.5; DB 1; Length 129;
 Best Local Similarity 62.18; Pred. No. 8.4e-33;
 Matches 82; Conservative 14; Mismatches 21; Indels 15; Gaps 3;
 QY 20 QVQLQDQAGLILKPEETLTCAVYGGSF--SGYWSWIRPPGKLEWIGENHSGSTN 77
 DB 1 RLOQESGPGIVKSEITSLTCIYSGGIRRTGYWGMIRPPKGLKLEWIGVYITGSIY 60
 QY 78 YNPGLKSRVITSDTSKNQFSKLSTVADTAVYICAREIAAPRHYE-----D 127
 DB 61 YNPFLRGRVITSDVTSRQFSILNLRMSADTAMYCAR---GNPPPYDIDIGTSDDSID 117
 QY 128 YWGQGLTVYSS 139
 DB 118 VMGQGTIVHVS 129
 RESULT 3
 HV46_MOUSE STANDARD; PRT; 137 AA.
 AC P01822;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION MOPC 315 PRECURSOR.
 OS Mus musculus (Mouse)
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 89238351.
 RA Rinfret A., Horne C., Dorrington K.J., Klein M.;
 RT "Cloning, sequencing and expression of the rearranged MOPC 315 VH
 gene segment.";
 RL Mol. Immunol. 26:431-434(1989).
 RN [2]
 RP SEQUENCE OF 1-31.
 RX MEDLINE: 78094475.
 RA Jilka R.L., Peetka S.;
 RT "Amino acid sequence of the precursor region of MOPC-315 mouse
 immunoglobulin heavy chain.";
 RL Proc. Natl. Acad. Sci. U.S.A. 74:5692-5696(1977).
 RN [3]
 RP SEQUENCE OF 1-21.
 RX MEDLINE: 79148758.
 RA Schechter I., Wolf O., Zemell R., Burstein Y.;
 RT "Structure and function of immunoglobulin genes and precursors.";
 RL Fed. Proc. 38:1839-1845(1979).
 RN [4]
 RP SEQUENCE OF 19-136.
 RX MEDLINE: 74170779.
 RA Francis S.R., Leslie R.G.O., Hood L., Eisen H.N.;

RT "Amino-acid sequence of the variable region of the heavy (alpha)
 RT chain of a mouse myeloma protein with anti-hapten activity.";
 RL Proc. Natl. Acad. Sci. U.S.A. 71:1123-1127(1974).
 RN [5]
 RP REVISION TO 53.
 RX MEDLINE: 77244979.
 RA Hood L., Margolies M.N., Givol D., Zakut R.;
 RT Unpublished results, cited by:
 RL Padlan E.A., Davies D.R., Peck I., Givol D., Wright C.;
 RL Cold Spring Harb. Symp. Quant. Biol. 41:627-637(1977).
 CC -1 MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
 CC PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
 CC -----
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 CC -----
 DR EMBL: M27638; AAA61337.1; -;
 DR EMBL: X07880; CAA30727.1; -;
 DR PIR: P0102; AVMS35.
 DR PFAM: PF00047; 1g; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 137
 FT DOMAIN 19 48
 FT DOMAIN 49 54
 FT DOMAIN 55 68
 FT DOMAIN 69 84
 FT DOMAIN 85 116
 FT DOMAIN 117 126
 FT DOMAIN 127 137
 FT DISULFID 40 114
 FT CONFLICT 15 15
 FT CONFLICT 15 15
 FT CONFLICT 77 78
 FT CONFLICT 102 102
 FT CONFLICT 123 123
 FT NON_TER 137 137
 SO SEQUENCE 137 AA; 15399 MW; FB3828304C2B81DC CRC64;
 Query Match 54.5%; Score 408; DB 1; Length 137;
 Best Local Similarity 60.38; Pred. No. 1.9e-32;
 Matches 85; Conservative 18; Mismatches 32; Indels 6; Gaps 4;
 QY 1 MKHLMEFLLLVAAPRWLVQVQLQDQAGLILKPEETLTCAVYGGSF--SGYWSWIRPP 59
 DB 1 MKVLSILYLITLAIIP-GIMSDVQLOESGPGIVKSEITSLTCSTGTSITSGYRWIRPP 59
 QY 60 PGKGLWIGENHSGSTNTPNSLKSRTVITSDTSKNQFSKLSTVADTAVYICAREIA 119
 DB 60 PGKLEWLGFIKYGDSNGVPSLKNRYSITRDSSENFILKNSVTEDTATYTCAGD-- 117
 QY 120 ARPH-REYDYGQGLTVYSS 139
 DB 118 -NDLTYFDYWGQGTIVHVS 137
 RESULT 4
 HV2G_HUMAN STANDARD; PRT; 117 AA.
 AC P01825;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-II REGION NEMM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

RN [1]
 RP SEQUENCE.
 RX MEDLINE: 77242302.
 RA Poljak R.J., Nakashima Y., Chen B.L., Konigsberg W.:
 RT "Amino acid sequence of the VH region of a human myeloma
 RL Immunoglobulin (IgG New)."
 RL Biochemistry 16:3412-3420(1977).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
 RX MEDLINE: 78066916.
 RA Saul F.A., Amzel L.M., Poljak R.J.:
 RT "Preliminary refinement and structural analysis of the Fab fragment
 RL from human immunoglobulin new at 2.0-A resolution."
 RL J. Biol. Chem. 253:585-597(1978).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
 CC PROTEIN.
 DR PIR: A02100; GIHUNM.
 DR PDB: 7FAB; 31-JAN-94.
 DR PFAM: PF00047; 19; 1.
 K Immunoglobulin V region; 3D-structure.
 F MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT NON_TER 117 117
 FT STRAND 3 7
 FT TURN 11 12
 FT TURN 14 15
 FT STRAND 18 25
 FT TURN 30 31
 FT STRAND 33 39
 FT TURN 41 42
 FT STRAND 46 51
 FT TURN 53 54
 FT STRAND 57 59
 FT TURN 61 63
 FT TURN 64 66
 FT TURN 72 72
 FT TURN 73 76
 FT STRAND 77 82
 FT TURN 87 89
 FT STRAND 91 98
 FT TURN 104 107
 FT STRAND 111 115
 SO SEQUENCE 117 AA; 12790 MW; 2DA47B509562D237 CRC64;

Query Match 53.1%; Score 397.5; DB 1; Length 117;
 Best Local Similarity 64.2%; Pred. NO. 1.6e-31;
 Matches 77; Conservative 19; Mismatches 21; Indels 3; Gaps 1;
 Db 20 OVOLOQMGAGLKPSETLSLTCAYVGGSGFYWSMTROPKGLGEMINHSSTNYN 79
 1 OVOLEQSGPLVRSQSLSLCTVSGSFSDYITWRQPKLEMLGIVFYHGISDPT 60
 QY 80 PSLSRVTISVDTSKNOFSKLSSVTADTAIVYVCARIEARPRRYDYMGOGTLVTVSS 139
 61 TPLRSRVTMLVDTSKNOFSKLSSVTADTAIVYVCARILN---GCLDYMGOGSLVTVSS 117
 RESULT 5
 HV60_MOUSE STANDARD; PRT; 116 AA.
 AC P18531;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION M315 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/CJ;
 RX MEDLINE: 89279149.
 RA Levy N.S., Malplero U.V., Lebecque S.G., Gearhart P.J.;

RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response."
 RL J. Exp. Med. 169:2007-2019(1989).
 DR PIR: J10509; HVMS31.
 DR PFAM: PF00047; 19; 1.
 K Immunoglobulin V region; Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 18
 FT DOMAIN 19 48
 FT DOMAIN 49 53
 FT DOMAIN 54 67
 FT DOMAIN 68 84
 FT DOMAIN 85 116
 FT DISULFID 40 114
 FT NON_TER 116 116
 SO SEQUENCE 116 AA; 13095 MW; 4562E03E53DC9E10 CRC64;

Query Match 49.5%; Score 370; DB 1; Length 116;
 Best Local Similarity 64.1%; Pred. No. 6.9e-29;
 Matches 75; Conservative 15; Mismatches 25; Indels 2; Gaps 2;
 Db 1 MKHLMPFLVAPRWYLSQVLOQMGAGLKPSETLSLTCAYVGGSGFYWSMTROP 59
 1 MKVLSLYLTLAIP-GILSDVQLQESGGLVPSQSLTSCSVTGYISGYNNMTROF 59
 QY 60 PKGLEWIGELINHSSTNYNPSLSKRTISVDTSKNOFSKLSSVTADTAIVYCAR 116
 60 PGNLEWNGYISYDGSNNYNPSLSKRTISVDTSKNOFSKLSSVTADTAIVYCAR 116
 Db 60 PGNLEWNGYISYDGSNNYNPSLSKRTISVDTSKNOFSKLSSVTADTAIVYCAR 116
 RESULT 6
 HV43_MOUSE STANDARD; PRT; 144 AA.
 AC P01819;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION MOPC 141 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 81012133.
 RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.:
 RT "Two types of somatic recombination are necessary for the generation
 RL of complete immunoglobulin heavy-chain genes."
 RL Nature 286:676-683(1980).
 CC -1- MISCELLANEOUS: THE SEQUENCE SHOWN IS TRANSLATED FROM A
 CC DIFFERENTIATED GENE ISOLATED FROM A MELOMA THAT SECRETES IGG2B.
 CC
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 CC
 DR EMBL: J00491; AAA38121.1;
 DR EMBL: Y00768; CAA24148.1;
 DR PIR: A02094; G2MS14.
 DR PFAM: PF00047; 19; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 144
 FT NON_TER 144 144
 SO SEQUENCE 144 AA; 15759 MW; 8E47A7CB3706D30A CRC64;

Query Match 49.4%; Score 369.5; DB 1; Length 144;
 Best Local Similarity 53.5%; Pred. No. 9.9e-29;

Matches 77; Conservative 21; Mismatches 41; Indels 5; Gaps 2;

QY 1 MKHMFELLVAPRWVLSOVLOQMGAGLKPSETLSITCAVYGGSGFYWSWIRPP 60
 DB 1 MAVTALLFLAFIPSCILSOVLKESGPGIVAPSOGLSTICVSGSLGVNWRPP 60
 QY 61 GGLGEWIGINHGSTNPNPSLKSRVTVISDTSKNOFSLKSVTAADTAAYVCAR---E 117
 DB 61 GGLGEWIGINHGSTNPNPSLKSRVTVISDTSKNOFSLKSVTAADTAAYVCAR---E 117
 QY 118 IAAHRHRY--DYNGOGITVTVSS 139
 DB 121 YGRSDKFTTLDYWGOGISVTVSS 144

RESULT 7

HV47_MOUSE
 ID HV47_MOUSE STANDARD: PRT: 113 AA.
 AC P01823;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION 36-60.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE.
 RC STRAIN-A/J;
 RX MEDLINE; 84024551.
 RA Juszczak E.C., Margolies M.N.;
 RT "Amino acid sequence of the heavy chain variable region from the A/J
 RT mouse anti-arsenate monoclonal antibody 36-60 bearing a minor
 RT idioType."
 RL Biochemistry 22:4291-4296(1983).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN ANTARSONATE
 CC MONOCLONAL ANTIBODY OF THE IGG2A SUBCLASS. IT REPRESENTS A SECOND
 CC IDIOTYPE FAMILY CHARACTERISTIC OF THE ANTARSONATE RESPONSE OF
 CC STRAIN A/J MICE.
 CC PIR: A02098; G2MS60.
 DR PFAM: PF00047; 1g; 1.
 DR Immunoglobulin V region: Antiarsonate antibody.
 FT NON_TER 113 113
 FT SEQUENCE 113 AA; 12734 MW; 38DC0EB3F5075B7 CRC64;

Query Match 48.1%; Score 359.5; DB 1; Length 113;
 Local Similarity 59.2%; Pred. No. 6.8e-28;
 Matches 71; Conservative 19; Mismatches 23; Indels 7; Gaps 1;

QY 20 QVLOQMGAGLKPSETLSITCAVYGGSGFYWSWIRPPGKLEWIGINHGSTNPN 79
 DB 1 EVOIQEGSGPVLKRSQSLSTLCVSTGSIISDYNNMRKFFGNLEMGITISYSGSTYIN 60
 QY 80 PSLKSRVTVISDTSKNOFSLKSVTAADTAAYVCAREIARPHRYDYNGOGITVTVSS 139
 DB 61 PSLKSRVTVISDTSKNOFSLKSVTAADTAAYVCAREIARPHRYDYNGOGITVTVSS 139

RESULT 8

HV02_XENLA
 ID HV02_XENLA STANDARD: PRT: 135 AA.
 AC P20957;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION XIG14 PRECURSOR (FRAGMENT).
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE; 86176921.
 RA Schwager J., Mikoryak C.A., Steiner L.A.;
 RT "Amino acid sequence of heavy chain from Xenopus laevis Igm deduced
 RT from cDNA sequence: implications for evolution of immunoglobulin
 RT domains."
 RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).

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DR EMBL; J03632; AAA49791.1;
 DR PIR; B31933; B31933.
 DR PFAM: PF00047; 1g; 1.
 KW Immunoglobulin V region: Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 18
 FT CHAIN 19 135 IG HEAVY CHAIN V REGION XIG14.
 FT NON_TER 135 135
 FT SEQUENCE 135 AA; 15080 MW; EBC467105C00732E CRC64;

Query Match 48.1%; Score 359.5; DB 1; Length 135;
 Best Local Similarity 54.5%; Pred. No. 8.3e-28;
 Matches 73; Conservative 19; Mismatches 39; Indels 3; Gaps 2;

QY 6 FFLVAPRWVLSOVLOQMGAGLKPSETLSITCAVYGGSGFYWSWIRPPGKLE 65
 DB 5 FIFMFSPSCILSOT-LOESGPETVAPKPSRLTCTVSGFEISYHMHWIRPPGKLE 63
 QY 66 WIGINHGSTNPNPSLKSRVTVISDTSKNOFSLKSVTAADTAAYVCAREIARHRY 125
 DB 64 WIGIANGGSLAIDSLKRVITIKDKNGKQVYLOQMGMEVKDTAMAYCARAYAGYN- 121
 QY 126 FDYWGOGITVTVSS 139
 DB 122 FDYWGOGITVTVSS 135

RESULT 9

HV61_MOUSE
 ID HV61_MOUSE STANDARD: PRT: 116 AA.
 AC P18532;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION IB43 PRECURSOR.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/CJ;
 RX MEDLINE; 89279149.
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 RT the primary immune response."
 RL J. Exp. Med. 169:12007-2019(1989).
 CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.
 CC PIR: J05058; HVM51B.
 DR PFAM: PF00047; 1g; 1.
 KW Immunoglobulin V region: Signal.
 FT SIGNAL 1 18
 FT CHAIN 19 116 IG HEAVY CHAIN V REGION IB43.
 FT DOMAIN 19 48 FRAMEWORK 1.
 FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 54 67 FRAMEWORK 2.
 FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 85 116 FRAMEWORK 3.

DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION J539.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP PRELIMINARY SEQUENCE.
RX MEDLINE; 79223895.
RA Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
immunoglobulin heavy chains from anti-galactan myeloma proteins and
its potential role in generating diversity in
complementarity-determining regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE; 88217852.
RA Suh S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,
RA Davies D.R.;
RT "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction
study at 2.6-A resolution.";
RL Proteins 1:74-80(1986).
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS GALACTAN.
CC PIR; A02080; AVMSJ5.
DR PDB; 2FBJ; 15-OCY-90.
DR PIR; A02080; AVMSJ5.
KW Immunoglobulin V region; 3D-structure.
FT NON_TER 119 119
FT STRAND 3 7
FT STRAND 10 12
FT TURN 14 15
FT STRAND 18 25
FT STRAND 29 31
FT HELIX 34 39
FT TURN 41 42
FT STRAND 45 51
FT TURN 53 54
FT STRAND 58 60
FT TURN 62 67
FT STRAND 68 72
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 100
FT TURN 101 103
FT STRAND 104 108
FT STRAND 112 116
FT SEQUENCE 119 AA; 13240 MW; 577BAF1DB675C1F1 CRC64;

Query Match 43.4%; Score 325; DB 1; Length 119;
Best Local Similarity 53.7%; Pred. No. 1.4e-24;
Matches 65; Conservative 19; Mismatches 33; Indels 4; Gaps 2;

OY 20 OVOLQWGMGLKPGSETSLTCAVYGGSPGYWMIROPGKGLWETGEIN-HSGSTNY 78
DB 1 EVKLESGGGLVQPGSLKSCAAGCFDFSKYMSWVRQAPGKGLWIGELHPSGTLNY 60
OY 79 NPSLSKRVITISYDTSKRNQFSLKLSVTADTAIVYCCAREIARPHRYEDYMGQGLTVTVS 138
DB 61 TPLSLDKRFLISHDNKNSLYLQMSKVRSEDTALYYCAR---LHYGYNAYMGQGLTVTVS 117
OY 139 S 139
DB 118 A 118

Search completed: July 26, 2000, 14:25:25
Job time: 1331 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2000, 14:01:29 ; Search time 48.79 Seconds
(without alignments)
197.529 Million cell updates/sec

Title: US-09-203-768A-2
Perfect score. 748

Sequence: 1 MKHLWFFLLVAPRWLSQ.....ARPHRYFDYWGQGLTVSS 139

Scoring table: BLOSUM62

Searched: 225878 seqs, 69334122 residues

Tc number of hits satisfying chosen parameters: 225878

```
Minimum DB seq length: 0
Maximum DB seq length: 10000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```

1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.oragnelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vterbrate:*
14: sp.unclassified:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	552	73.8	150	4	095973	095973 homo sapien
2	328.5	43.9	82	4	075725	075725 homo sapien
3	312	41.7	78	4	075739	075739 homo sapien
4	304	40.6	147	4	095709	095709 homo sapien
5	296.5	39.6	75	4	075743	075743 homo sapien
6	287		38.4	11	0951C4	0951C4 mus musculen
7	278.5	37.2	88	4	075737	075737 homo sapien
8	269.5	36.0	117	11	0951C6	0951C6 mus musculen
9	264.5	35.4	150	4	095729	095729 homo sapien
10	256.5	34.3	157	4	095738	095738 homo sapien
11	245	32.8	97	4	043334	043334 homo sapien
12	224.5	30.0	77	4	075741	075741 homo sapien
13	216.5	28.9	78	4	075730	075730 homo sapien
14	208	27.8	80	4	075727	075727 homo sapien
15	203.5	27.2	82	4	075729	075729 homo sapien
16	201.5	26.9	80	4	075735	075735 homo sapien
17	198	26.5	77	4	075732	075732 homo sapien
18	195	26.1	82	4	075726	075726 homo sapien
19	192.5	25.7	78	4	075723	075723 homo sapien

20	191.5	25.6	81	4	075721	homo sapien
21	190	25.4	81	4	075719	homo sapien
22	189	25.3	77	4	075728	homo sapien
23	185.5	24.8	79	4	075711	homo sapien
24	181.5	24.3	76	4	075742	homo sapien
25	180.5	24.1	72	4	075740	homo sapien
26	176.5	23.6	86	4	075748	homo sapien
27	175.5	23.5	81	4	075734	homo sapien
28	175.5	23.5	86	4	075722	homo sapien
29	173.5	23.2	78	4	075720	homo sapien
30	171.5	22.9	74	4	075740	homo sapien
31	162.5	21.7	76	4	075733	homo sapien
32	155	20.7	81	4	075736	homo sapien
33	113.5	15.2	145	13	09YH09	ginglymasto
34	111	14.8	64	11	061750	mus masculin
35	108	14.4	135	13	09YH19	ginglymasto
36	107.5	14.4	136	13	09YH16	ginglymasto
37	107	14.3	136	13	09YH69	ginglymasto
38	105	14.0	142	13	09YH63	ginglymasto
39	104	13.9	122	4	099603	homo sapien
40	103	13.8	122	4	099604	homo sapien
41	101.5	13.6	38	4	015224	homo sapien
42	101.5	13.6	129	13	09YH1	ginglymasto
43	101.5	13.6	143	13	09YH13	ginglymasto
44	101	13.5	134	13	09YH17	ginglymasto
45	101	13.5	136	13	09YH14	ginglymasto

ALIGNMENTS

RESULT	1		
095973			
ID	095973	PRELIMINARY;	PRT; 150 AA.
AC	095973;		
DT	01-MAY-1999, (Tremblrel, 10, Created)		
DT	01-MAY-1999 (Tremblrel, 10, last sequence update)		
DT	01-NOV-1999 (Tremblrel, 12, last annotation update)		
DE	VAR4 HEAVY CHAIN VARIABLE REGION PRECURSOR (FRAGMENT).		
GN	IGM.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;		
CC	Eutheria; Primates; Catarrhini; Homidae; Homo.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	SUH C.-H., SONG C.-H., LEE C.-H., LEE S.-K.;		
RT	"Clonal proliferation of IGM secreting B cell in the synovium of		
RL	Behcet's patient with arthritis."		
DR	Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.		
DR	EMBL; AF103795; AAC79084.1; -		
DR	HSSP; P01825; 7FAB.		
KW	signal.		
FT	SIGNAL	1 19	POTENTIAL.
FT	CHAIN	20 >150	VAR4 HEAVY CHAIN VARIABLE REGION.
FT	NON_TER	150	
Q0	SEQUENCE	150 AA; 16315 MF; 508A92A6 CRC32;	

Query Match Similarity	73.8%	Score 552	DB 4	Length 150
Best Local Similarity	76.8%	Pred. No. 4.2e-49		
Matches 109	Conservative 11	Mismatches 14	Indels 8	Gaps 3

QY	1	NKHLMEFLLVAPRMYLSQVLOQMGAGLKPSETLSLTCAVYGGSFSS-GYWSMIHQ	58
DB	1	NKHLMEFLLVAPRMYLSQVLOQMGAGLKPSETLSLTCAVYGGSSISTNYMGWIMQ	60
QY	59	PPGKLEWIGELINHGSGSTINYPNPSLSRVTISVDTSKNQPSKLSSVTAADTAVYICAR-E	117
DB	61	PPKLEWIGSLHNGSGSDYINPNSLSRVTISVDTSKNQPSKLSSVTAADTAVYICARLG	120
QY	118	IAARPHRYFDYMGQGLTVYSS	139
DB	121	MGA----FDENGHGIMTVSS	137

RESULT 2
ID 075725 PRELIMINARY; PRT; 82 AA.
AC 075725;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-INTERESTINE;
RA FISCHER M., KUEPPERS R.;
RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
mutated VH region genes."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: A0009522; CA08729.1; -.
DR HSSP: P01825; 7FAB. 1
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 9566 MW; 1F2E1379 CRC32;

Query Match 43.98; Score 328.5; DB 4; Length 82;
Best Local Similarity 74.48; Pred. No. 1.3e-26;
Matches 61; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

OY 49 GGYWMIROPKGLWIGLHSGSTNPNPSLKSRTYISVDSKNOFSLKSTYAAD 108
Db 1 SREWMIROPKGLWIGLHSGSTNPNPSLKSRTYISVDSKNOFSLKSTYAAD 60
OY 109 TAVYCARPFGGRAMPYFDY 129
Db 61 TAVYCARPFGGRAMPYFDY 82

RESULT 3
ID 075739 PRELIMINARY; PRT; 78 AA.
AC 075739;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE 3 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-INTERESTINE;
RA FISCHER M., KUEPPERS R.;
RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
mutated VH region genes."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: A0009538; CA08743.1; -.
FT NON_TER 78 78
SQ SEQUENCE 78 AA; 9031 MW; 05D273B9 CRC32;

Query Match 41.78; Score 312; DB 4; Length 78;
Best Local Similarity 74.48; Pred. No. 5.8e-25;
Matches 58; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
OY 52 YWMIROPKGLWIGLHSGSTNPNPSLKSRTYISVDSKNOFSLKSTYAADTAV 111
Db 1 YWMIROPKGLWIGLHSGSTNPNPSLKSRTYISVDSKNOFSLKSTYAADTAV 60

OY 112 YFCARHSSWPIYFDNW 129
Db 61 YFCARHSSWPIYFDNW 78

RESULT 4
ID 095509 PRELIMINARY; PRT; 147 AA.
AC 095509;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
DE VH3 PROTEIN (FRAGMENT).
GN VH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96071149.
RA CAO J., VESCTO R.A., RETTIG M.B., HONG C.H., KIM A., LEE J.C.,
LICHTEINSTEIN A.K., BERENSON J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
myeloma using PCR with patient-specific immunoglobulin gene primers."
RL Leukemia 9:1948-1953(1995).
DR EMBL: S80860; AAD14339.1; -.
FT NON_TER 1 1
SQ SEQUENCE 147 AA; 15768 MW; BDD8F70 CRC32;

Query Match 40.68; Score 304; DB 4; Length 147;
Best Local Similarity 48.18; Pred. No. 8.1e-24;
Matches 63; Conservative 20; Mismatches 32; Indels 16; Gaps 3;

OY 20 QVQLQQWAGLILPSETLSLTCAVYGGSPFGYWMIRPPKGLWIGLHSGSTNPN 79
Db 1 QVHLVESGGGVQPGKSLRSCASGFTSTYGMVNRQAPGLDMVALISYDSGY 60
OY 80 P-SLKSRTYISVDSKNOFSLKSTYAADTAVYCARPFGGRAMPYFDY 128
Db 61 AGSVKGRFTISRDNSKNTLYLQMTSLRVEDTAVYCAKD---GNYPFSGVGYAGIDY 115
OY 129 WGGGLTVTVSS 139
Db 116 WGGGLTVTVSS 126

RESULT 5
ID 075743 PRELIMINARY; PRT; 75 AA.
AC 075743;
DT 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-INTERESTINE;
RA FISCHER M., KUEPPERS R.;
RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
mutated VH region genes."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: A0009543; CA08747.1; -.
FT NON_TER 75 75
SQ SEQUENCE 75 AA; 8667 MW; 8D5C330F CRC32;

```

Query Match 39.6%; Score 296.5; DB 4; Length 75;
Best Local Similarity 71.8%; Pred. No. 2.1e-23;
Matches 56; Conservative 6; Mismatches 13; Indels 3; Gaps 1.

OY 52 YWSWIRPPGKGLWIGELINHSNSTNYNSLSKRVYISVDTSKNOFSLKSYTADTAV 111
Db 1 YWATIRPPGKGLWIGELINHSNSTNYNSLSKRVYISVDTSKNOFSLKSYTADTAV 60
OY 112 YYCAREIARPHRYFDYW 129
Db 61 YYCARR--HGYSWEDPW 75

RESULT 6
O921C4 PRELIMINARY; PRT; 118 AA.
O921C4
AC O921C4;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
Db ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RA MUELLER J.P., GIANNONI M.A., HARTMAN S.T., ELLIOTT E.A., SOUINTO S.P.,
RA MATIS L.M., EVANS M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT 19g2/64 constant regions block human leukocyte binding to porcine
RT endothelial cells."
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
DR EMBL; U78801; AAD00293.1; -.
FT NON_TER 1 1
FT NON_TER 1 118
SO SEQUENCE 118 AA; 13036 MW; 45653221 CRC32;

Query Match 38.4%; Score 287; DB 11; Length 118;
Best Local Similarity 45.5%; Pred. No. 3.4e-22;
Matches 55; Conservative 23; Mismatches 39; Indels 4; Gaps 2.

OY 20 OYOLOQMGAGLKPSETLSLTCAYVGGSGFYWSNIRPPKGLWIGELI-NHSGSTNY 78
Db 1 OYOQOAGELARPMASVYKLSKASGYNNSYWMQVQKPGGGLWICAIYPGDDTGY 60
OY 79 NPSLSRVYISVDTSKNOFSLKSYTADTAVYYCAREIARPHRYFDYWGGLTYVS 138
Db 61 TOKFPGKATLTADKSSSTAYMOLSLSPASDSAYVCARRTVG---GYFDYWGGLTYVS 117

OY 139 S 139
Db 118 S 118

RESULT 7
O75737 PRELIMINARY; PRT; 88 AA.
O75737
AC O75737;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 12, Last annotation update)
DE VH HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-INTESTINE;
RA FISHER M., KUEPERS R.;
RT "Human Iga and Igm secreting intestinal plasma cells carry heavily

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RT      mutated VH region genes."
RL      Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AJ0069535; CAA08741.1; -.
DR      HSSP; P01825; 7FAB.
FT      NON_TER          1
FT      NON_TER          1
SQ      SEQUENCE        88 AA; 10088 MW; C76DC923 CRC32;

Query Match
Best Local Similarity    37.2%; Score 278.5; DB 4; Length 88;
Matches    53; Conservative    11; Mismatches    14; Indels    9; Gaps    2

OY      52 YWSRTPGPGKGLGVIGTGINHSGSTNNVPSLSKRYTISVDTSKNQFSKLSSVTADNAV 111
       ::::|||||:::::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB      2 WWTWVRQAPGRGLEIIGEIVGGDTNPNPSLKGRLLTLIDKSMNQFSLIRSVTAADSAY 61

OY      112 YYCARE-----IAARHRVF----DYW 129
       |||||         |:::|||         |
DB      62 YYCARGGGYHCIGGRCRYNYNGVDYW 88

RESULT      8
O9Z1C6      PRELIMINARY; PRT; 117 AA.
AC          O9Z1C6;
DT      01-MAY-1999 (TREMBLrel. 10, Created)
DM      01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT      01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE      ANTI-PORCINE VCAM NAB 2A2 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Mammalia;
OC      Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-BALB/C;
RA      MOELLER J.P., GIANNONI M.A., HARTMAN S.L., ELLIOTT E.A., SOUINIO S.P.,
RA      MATIS L.M., EVANS M.J.;
RT      "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT      IgG2/G4 constant regions block human leukocyte binding to porcine
RT      endothelial cells."
RL      Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; U78799; AAD00291.1; -.
FT      NON_TER          1
FT      NON_TER          1
SQ      SEQUENCE        117 AA; 13122 MW; DC234181 CRC32;

Query Match
Best Local Similarity    36.0%; Score 269.5; DB 11; Length 117;
Matches    55; Conservative    23; Mismatches    37; Indels    7; Gaps    3;

OY      20 QYOLOQMAGLKRPEETLSLCNAVYGGSFGSYGMWINQPPKRGLEIGELNHSGS-TNY 78
       |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB      1 QVOLOQSPQLVPRPTSVKXISCAGSYFTSYMMHWKRPQODELMIPDSSEVL 60

OY      79 NPSLSRVLTISVDTSKNQFSKLSSVTADTVYYICAR-EIARPHRYPDYMGCGTLYTV 137
       |:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
DB      61 NORLKDRIILTYDKSNSNIAYNMQFSPTSEDSAVYICTRGEVS-----WFATYMGCGITLVY 115

OY      138 SS 139
       ::
DB      116 SA 117

RESULT      9
O9Y298      PRELIMINARY; PRT; 150 AA.
AC          O9Y298;
DT      01-NOV-1999 (TREMBLrel. 12, Created)
DT      01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT      01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE      IGG VH PROTEIN PRECURSOR (FRAGMENT)".
```

GN IGG VH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 98322155.
 RA JACQUEMIN M.G., VANDER ELST L.P.L.;
 RT "Mechanism and kinetics of factor VIII inactivation: study with an
 RT IgG4 monoclonal antibody derived from a hemophilia A patient with an
 RT inhibitor".
 RL Blood 92:496-506(1998).
 DR EMBL: AJ224083; CAAL1829.1; -.
 KW Signal.
 FT SIGNAL.
 FT NON-TER 1 19 POTENTIAL.
 SQ SEQUENCE 150 AA; 16031 MW; B18EC39A CRC32;

Query Match
 Best Local Similarity 35.4%; Score 264.5; DB 4; Length 150;
 Matches 61; Conservative 21; Mismatches 53; Indels 5; Gaps 3;

QY 1 MKHLWPELLVAAPRWYLSQVLOQWAGLLKPSSETLTCAYVGSFSGYTWIRPP 60
 DB 1 MDMTWKLEFLVAAATGTHAOLVDSGAVYKKGASVYKSGYTLTELPVHWGAP 60
 QY 61 GKLEWIGEIN-HSGSTNPNLSKRVTSVDSKNOFSLKSTVAADTAVYCCARETA 119
 DB 61 GKLEWGSFDESGESITAREFGSVTADTIDIAVMELSLSDTAVYCCA---V 117
 QY 120 ARPHRYFDYWGQGLTVYSS 139
 DB 118 PDPDA-FDIMGGTMYTVSS 136

RESULT 10
 ID 095978 PRELIMINARY; PRT; 157 AA.
 AC 095978;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DE 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE VH1 PROTEIN PRECURSOR (FRAGMENT).
 GN VH1.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PERIPHERAL BLOOD;
 RA JOX A., ZANDER T., KUEPPERS R., IRSCH J., KANZLER H., KORNACKER M.,
 RA BOHLEN H., DIEHL V., WOLF J.;
 RT "Absence of immunoglobulin in Hodgkin-Reed Sternberg cells of a
 RT patient with mixed cellularity Hodgkin's disease is associated with
 RT somatic mutations within the untranslated regions of rearranged and
 RT class switch recombinated Ig genes".
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ005570; CAA06599.1; -.
 KW Signal.
 FT SIGNAL.
 FT NON-TER 1 21 POTENTIAL.
 SQ SEQUENCE 157 AA; 17304 MW; 88468024 CRC32;

Query Match
 Best Local Similarity 34.3%; Score 256.5; DB 4; Length 157;
 Matches 61; Conservative 19; Mismatches 58; Indels 3; Gaps 3;

QY 1 MKHLWPELLVAAPRWYLSQVLOQWAGLLKPSSETLTCAYVGSFSGYTWIRPP 59
 DB 1 MDMTWKLEFLVAAATGTHAOLVDSGAVYKKGASVYKSGYTLTELPVHWGAP 59

QY 60 PKGLEWIGEINHS-GSTNPNLSKRVTSVDSKNOFSLKSTVAADTAVYCCAREI 118
 DB 60 PKGLEWGSFDESGESITAREFGSVTADTIDIAVMELSLSDTAVYCCAREI 119
 QY 119 ARPHRYFDYWGQGLTVYSS 139
 DB 120 ARSGYNGHMGQGPVYSS 140

RESULT 11
 ID 043234 PRELIMINARY; PRT; 97 AA.
 AC 043234;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DE 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE RHEUMATOID FACTOR RF-ET13 (FRAGMENT).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA BORRETTEN M., NATVIG J.B., THOMPSON K.M.;
 RL Mol. Immunol. 0:0-0(1997).
 DR EMBL: AF035802; AAB8534.1; -.
 DR PFAV: PF00047; 19; 1.
 FT NON-TER 1 1
 FT NON-TER 97 97
 SQ SEQUENCE 97 AA; 10748 MW; EC95D20C CRC32;

Query Match
 Best Local Similarity 32.8%; Score 245; DB 4; Length 97;
 Matches 50; Conservative 16; Mismatches 28; Indels 2; Gaps 1;

QY 23 LQWAGLLKPSSETLTCAYVGSFSGYTW--SWIRPPKGLEWIGEINHSSTNPNP 80
 DB 2 LKESPALVKNPTETLTLCYVSGFSLNRKGVSWIRPPKRAVWLAHIFANDEKSI 61
 QY 81 SKSRVTSVDSKNOFSLKSTVAADTAVYCCAR 116
 DB 62 SLKSRVTSVDSKNOFSLKSTVAADTAVYCCAR 97

RESULT 12
 ID 075741 PRELIMINARY; PRT; 77 AA.
 AC 075741;
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
 GN VH.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-INTESTINE;
 RA FISCHER M., KUEPPERS R.;
 RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
 RT mutated VH region genes".
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ009540; CAA08745.1; -.
 DR HSSP: P01772; 2162.
 FT NON-TER 1 1
 FT NON-TER 77 77
 SQ SEQUENCE 77 AA; 8734 MW; 1F7F9E8E CRC32;

Query Match
 Best Local Similarity 30.0%; Score 224.5; DB 4; Length 77;
 Matches 48; Conservative 6; Mismatches 16; Indels 11; Gaps 3;

```

OY 54 SWIRPAPGGLMEIGWELINHSSTN-TYNPPLKSRVITSDTSKNQPSLKSSTVADTAY 112
    ||| ||||| : : : | : | : | : | : | : | : | : | : | : | : | : |
DB   3 SWVRAPAGGLEMGWSIGSSGDYTYADSVKGRFTISRDNKNTLSLTQLNSTAEDTAY 62
    |||      -|-      EDYW 129
    |||      -|-      EDYW 77
OY 113 YCARFIARPHRY----EDYW 129
    |||      -|-      EDYW 77
DB   63 YCAR-----HYDSSPFEDYW 77

RESULT 13
ID 075730 PRELIMINARY: PRT: 78 AA.
AC 075730:
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-NOV-1998 (TREMBLrel. 12, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-INTESTINE:
RA FISHER M., KUEPPERS R.;
RT "Human Iga and IGM secreting intestinal plasma cells carry heavily
RL mutated VH region genes.";
RZ Submitted (JUL-1998) to the EMBL/genbank/DBJ databases.
DR EMBL; AJ009527; CAA08734.1; -.
DR HSSP; P01772; 2IG2.
FT NON_TER 1 1
FT NON_TER 78 78
SQ SEQUENCE 78 AA; 8994 MW; 0A3BF0E5 CRC32;

Query Match 28.9%; Score 216.5; DB 4; Length 78;
Best Local Similarity 49.4%; Pred. No. 3,2e-15;
Matches 40; Conservative 16; Mismatches 20; Indels 5; Gaps 2;

OY 50 GYWSMWRPCKGGLMEIGWELINHSSTN-YNPSPKSRVITSDTSKNQPSLKSSTVAD 108
    ||:||||| |||||::||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB   2 GWMSMWVRAPAGGLEMGWVNINEDSGKYTDVSKGRFTILDSANNSLTQLMTLRAD 61
    |||:|||::: : : ||||

OY 109 TAVYYCARFIARPHRYEDYW 129
    |||:|||::: : : ||||
DB   62 TAVYHCARDV-----NGHFDYW 78

RESULT 14
ID 075727 PRELIMINARY: PRT: 80 AA.
AC 075727:
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE 01-NOV-1998 (TREMBLrel. 12, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-INTESTINE:
RA FISHER M., KUEPPERS R.;
RT "Human Iga and Igm secreting intestinal plasma cells carry heavily
RL mutated VH region genes.";
RZ Submitted (JUL-1998) to the EMBL/genbank/DBJ databases.
DR HSSP; P01772; 2IG2.
FT NON_TER 1 1
FT NON_TER 80 80
SQ SEQUENCE 80 AA; 9351 MW; 63DE15BA CRC32;

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Query Match          27.8%; Score 208; DB 4; Length 80;
Best Local Similarity 51.9%; Pred. No. 2,4e-14;
Matches 42; Conservative 10; Mismatches 25; Indels 4; Gaps 2

QY 52 YWSMIRPGPGKLEWIGELIN--HSGSTNYNSLSKRVITISVTSKQPSLKSSTYAAD 108
   | : | | | | | | | | | | : | | | | | | | | | | | : | | | |
Db 1 YVDWVRQAPGKLEWVGRKRKANKSYTTEYASVSGRFTISRDSDKNSLYLQNTLRADT 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 109 TAVYTCAREIARPHRYFDYW 129
   | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 TAVYTCARD-HLRSAAYFDLW 80
   | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 15
ID 075729 PRELIMINARY; PRT; 82 AA.
AC 075729;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
NC (1)
NM RP SEQUENCE FROM N.A.
RC TISSUE=INTESTINE;
RT FISCHER M., KUEPPERS R.;
RA "Human Iga and Igm secreting intestinal plasma cells carry heavily
RL mutated VH region genes.";
RL Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ009526; CAA08733.1; -.
DR HSSP; P01772; 2IG2.
FT NON-TER 1
FT NON-TER 82
SQ SEQUENCE 82 AA; 9396 MW; 9063B32A CRC32;

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Search completed: July 26, 2000, 14:25:01
Job time: 1412 sec

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Query Match Similarity      27.2%: Score 203.5: DB 4: Length 82:
Best Local Similarity      50.0%: Pred. No. 7,2e-14:
Matches      41: Conservative      12: Mismatches      26: Indels      3: Gaps      2

QY      51 YYWSMIRDPGKGLEWIGETINHSG-STNTNPSLKSRYTISVDTSKNQFSLKISSVTADT 109
      | : : : | | | | | : : : | | | | | | | | | | : : : : | |
DB      1 YAMSWWRQAPGKGLEWVSSIDGAGIDITYAESYKGRFTISRDNKNTLYLQWNTLRAEDT 60

QY      110 AVYYCARE--IAARPHRYFDYW 129
      | | | | : : | | | |
DB      61 AVYYCVKDGVSANSWMDYFDYW 82

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 26, 2000, 14:01:26 ; Search time 33.21 Seconds

(without alignments)
83.447 Million cell updates/sec

Title: US-09-203-768a-4
Perfect score: 615

Sequence: 1 LMLPDTGTEIVMTQSPATLS.....QYNMPPYTFGQTKLEIKR 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	538.5	87.6	234	1 R52951	Human anti-IgE MAb
2	523	85.0	129	1 R38672	VK325-Jk2. DNA seq
3	518	84.2	117	1 W47582	Human monoclonal a
4	513.5	83.5	349	1 R12128	1B1 IgG aberrant 1
5	513.5	83.5	414	1 R13018	1B1 IgG aberrant 1
6	513.5	83.5	414	1 R13111	1B1 IgG aberrant 1
7	509.5	82.8	214	1 Y06842	Seq ID No:10 of JP
8	504.5	82.0	134	1 W11155	Anti-lung tumour a
9	499	81.1	129	1 R41286	F105 rearranged va
10	497	80.8	129	1 R38673	F105VK-F105JK. DNA
11	494	80.3	150	1 W40069	Human monoclonal a
12	493.5	80.2	401	1 R12129	ORF 1 of IgE light
13	490.5	79.8	127	1 W08946	Kappa V-light chain
14	489	79.5	115	1 R38648	Human V-kappa frag
15	489	79.5	115	1 R62928	Human V-kappa vk65
16	489	79.5	115	1 W41144	Human vkappa65.3 f
17	489	79.5	115	1 W62182	Human DNA vkappa65
18	480	78.0	124	1 W24539	Immunoglobulin r10
19	476.5	77.5	120	1 W03946	DNA fragment vk65.
20	475.5	77.3	127	1 R50192	Light chain variab
21	474.5	77.2	109	1 W84095	Human v-kappa subg
22	474	77.1	110	1 W27545	Human Ab light cha
23	469.5	76.3	127	1 R50187	Light chain variab
24	469.5	76.3	128	1 P91001	Anti-P. aeruginosa
25	466.5	75.9	127	1 R50191	Light chain variab
26	465	75.6	115	1 R38649	Human V-kappa frag
27	465	75.6	115	1 R62929	Human V-kappa vk65
28	465	75.6	115	1 W03947	DNA fragment vk65.
29	465	75.6	115	1 W41145	Human vkappa65.5 f
30	465	75.6	115	1 W62183	Human DNA vkappa65
31	463.5	75.4	116	1 R38650	Human V-kappa frag
32	463.5	75.4	116	1 R62930	Human V-kappa vk65
33	463.5	75.4	116	1 W03948	DNA fragment vk65.

34	463.5	75.4	116	1 W41146	Human vkappa65.8 f
35	463.5	75.4	116	1 W62184	Human DNA vkappa65
36	458	74.5	107	1 R54308	Anti-HIV gp120 imm
37	458	74.5	107	1 W01266	VL region of HIV n
38	457.5	74.4	105	1 W31725	Alpha light chain
39	453.5	73.7	107	1 R38593	Human lambda light
40	453.5	73.7	107	1 W58493	Human kappa light
41	453.5	73.7	109	1 R50218	HSV glycoprotein F
42	453.5	73.7	238	1 W83034	Anti-Fas humanised
43	452	73.5	287	1 W40071	Human H11-scFv con
44	452	73.5	304	1 W40070	Human H11-scFv con
45	449	73.0	108	1 R54316	Anti-HIV gp120 imm

ALIGNMENTS

RESULT 1	
ID R52951	R52951 standard; Protein; 234 AA.
AC R52951	
DT 27-OCT-1994	(first entry)
DE Human anti-IgE MAb light chain.	
KW Human IgE; CH4 region; triggers mediator release;	
KM Mast cells; Monoclonal antibody; allergy.	
OS Homo sapiens.	
FT Key	Location/Qualifiers
FT region	21..128
FT	/label= light chain variable region
PN EP-592230-A.	
PD 13-APR-1994.	
PF 07-OCT-1993	308006.
PR 07-OCT-1992	JP-283800.
PA (SNOW) SNOW BRAND MILK PROD CO LTD.	
PI Goto M, Kobayashi F, Mizuno A, Morinaga T, Washida N;	
PI Yoshida T;	
DR WPI; 94-120330/15.	
DR N-PSDB: 071872.	
PT Human monoclonal anti-IgE peptide antibody - inhibits histamine	
PT release from mast cells by allergen stimulation, useful for	
PT preventing allergies	
PS Claim 3; Page 12; 21pp; English.	
CC R52951 shows the light chain of a human type anti-IgE peptide	
CC monoclonal antibody which inhibits the signal transmission for	
CC the release of chemical mediator from mast cells and basophils	
CC stimulated with allergen. The antibody can be used for the	
CC prophylaxis and the therapy of allergy.	
SC Sequence 234 AA;	
Query Match	87.6%; Score 538.5; DB 1; Length 234;
Best Local Similarity	87.9%; Pred. No. 2.5e-33;
Matches 102; Conservative	9; Mismatches 4; Indels 1; Gaps 1;
OY 1	LMLPDTGTEIVMTQSPATLSVSPGERATLSCRASQSVSNLYAQQKPGAPRLITYGAS 60
DB 13	LMLPDTGTEIVMTQSPATLSVSPGERATLSCRASQSVSNLYAQQKPGAPRLITYGAS 72
OY 61	TRATGTPARSSGSGSGTEFLTITSSLSQSEDFAYVYCOQYNNMPPYTFGQTKLEIKR 116
DB 73	TRATGTPARSSGSGSGTEFLTITSSLSQSEDFAYVYCOQYNSM-PRFPGQTKYDLK 127
RESULT 2	
ID R38672	R38672 standard; Protein; 129 AA.
AC R38672	
DT 01-NOV-1993	(first entry)
DE VK325-Jk2.	
KW Monoclonal antibody; MAb; envelope; glycoprotein; gp120; HIV; AIDS;	
KM CD4; receptor; hydridoma; polymerase chain reaction; PCR; heavy; light;	
KW chain; epitope; immune deficiency.	
OS Homo sapiens.	

FH	Key		Location/Qualifiers	
FT	peptide		1..20	
FT		/label= sig_peptide	21..129	
FT	protein		/label= mat_protein	
FT		/label= vk325	1..116	
FT	region		/label= Jk2	
FT		/label= CDRI	71..77	
FT	region		/label= CDR2	
FT		/label= CDR3	110..117	
FT	misc_difference	1	/note= "Met encoded by ATC (sic)"	
FT		/note= "Pro encoded by GCA (sic)"	35	
FT	misc_difference	99	/note= "Leu encoded by GTG (sic)"	
FT		/note= "Gly encoded by GAT (sic)"	113	
FT	misc_difference	114	/note= "Ser encoded by AAC (sic)"	
FT		/note= "Pro encoded by GTT (sic)"	116	
FN	WO312232-A.			
PD	24-JUN-1993.			
PF	10-DEC-1992:	U10928.		
PR	10-DEC-1991:	US-804652.		
PA	(DAND) DNA FARBER CANCER INST INC.			
DRA	(NEW)- NEW ENGLAND DEACONNESS HOSPITAL CORP.			
PI	Haseilne WA, Marasco WA, Posner MR, Sodroski JG;			
DR	N-PSTDB; Q42706.			
PT	DNA segments encoding monoclonal antibody - which binds to gp120			
PS	and neutralises HIV, for treating AIDS, and for diagnosing and			
PL	monitoring HIV infection			
CC	Dislosure; Page 74-75; 109pp; English.			
CC	The nucleotide sequence of F105 VK (Q42707 - sequence differs from			
CC	other F105 VK sequences given elsewhere in the specification) was			
CC	compared with gemline gene HumvK325 (Q42706), showing 97.7% similarity.			
CC	By nucleotide sequence analysis, F105 appears to			
CC	be derived from a member of the VK III subgroup gene family.			
SQ	Sequence 129 AA;			
OY	Best Local Similarity	85.0%; Score 523; DB 1; Length 129;		
bB	Matches 103; Conservative	87.3%; Pred. No. 2e-33; Mismatches 6; Indels 2; Gaps		
OY	1 LMLPTTGELIVMTGPSALISVSGPERATISCASOSVSNN-LAWYOQGAPRLLIYG A	59		
bB	13 LMLPTTGELIVLTQSGLITSLSPGERATISCASOSVSNTLAWYOQKGAPRLLIYG A	72		
Db	60 STRATIGARFESGSNGTEFLTLISSLOEDRAYVCQQYNMPPTFEGGRLEIK R	117		
	73 SSRATIGDFRSFGSNGIDFTLIIRLPEDRAYVICQQYS-SPTFEQGRLEIK R	129		
RESULT	3			
ID	W47582 standard; Protein; 117 AA.			
DT	W47582; 22-JUN-1998 (first entry)			
KD	Human monoclonal antibody light chain variable region.			
RN	Human; monoclonal antibody; hybridoma cell strain Tt6c; hMAb;			
RT	antitetaus toxin.			
OS	Homo sapiens.			
FT	key Location/Qualifiers			
FT	Region 24..34 /label= CDRI			

FT	Region		49..55	/label= CDR2
FT	Region		69..98	/label= CDR3
FT	J100I4570-A.			
PD	20-JAN-1998.			
PF	05-JUL-1996.		194095.	
PR	05-JUL-1996; JP-194095.			
PA	(MATSU) MATSUDA M.			
PA	(MOMI) MORINAGA & CO LTD.			
DR	WPI: 98-138233/13.			
DR	N-PDSB: V18674.			
PT	New cDNA encoding human monoclonal antibody - useful for production			
PT	of antibody by hybridoma techniques commercially			
PS	Claim 4; Fig 2; 8pp; Japanese.			
CC	The present sequence represents a human monoclonal antibody (hmab)			
CC	light chain variable region. The cDNA encoding the hmab can be used			
CC	for commercial production of the hmab. The cDNA was isolated from an			
CC	antileukemia toxin human monoclonal antibody producing hybridoma cell			
CC	strain VTG6.			
SQ	Sequence 117 AA;			
Query Match		84.2%; Score 518; DB 1; Length 117;		
Best Local Similarity		90.8%; Pred. No. 4,3e-32;		
Matches	99; Conservative	6; Mismatches	4; Indels	0; Gaps
OY	9 EIVMTSPATISVSGEANTLSCRAOSVSNTLAWYOOKPGQAPRLTYGASTRATGIPA 68			
Dd	1 DIVMTSPATISVSGEANTLSCRAOSVSNTLAWYOOKPGQAPRLTYGASTRATGINA 60			
OY	69 RFSGGSGTEFTLTITSSLOSEDFAVYYCOQYNMPDPYTFGGCTKLEIKR 117			
Dd	61 RFSGGSGTEFTLTITSSLOSEDFAVYYCOQYSMDPQRFEGGTKEIRR 109			
RESULT 4				
ID	R12128 standard; Protein; 349 AA.			
AC	R12128;			
DT	01-AUG-1991 (first entry)			
KW	1b1 igg aberrant light chain with duplicated variable region.			
KW	immunoglobulin G; light chain; variable region; duplication;			
KW	passive immunity; group B streptococci.			
CS	Homo sapiens.			
FH	Key			
FT	Location/Qualifiers			
FT	peptide		1..17	
FT	/label= leader peptide		18..130	
FT	region		/label= variable region	
FT			/note= "LV 1"	
FT	region		131..243	
FT			/label= variable region	
FT			/note= "LV 2"	
FT	region		244..345	
FT			/label= constant region	
FN	MOJ106305-A.			
PD	16-MAY-1991.			
PE	06-NOV-1980; U06426.			
PR	07-NOV-1989; US-432700.			
PA	(BRIM) BRISTOL-MYERS SQUIB.			
PI	Shuford WW, Harris LJ, Raif HV;			
PI	WPI: 91-163947/22.			
DR	N-PDSB: O1878.			
PT	Oligomeric immunoglobulin(s) with high avidity for antigen(s) -			
PT	formed by duplicating esp. variable region of light chain of IgG			
PT	Class "			
PS	Example 5; Fig 16; 104pp; English.			
CC	This sequence is deduced from the cDNA clone 4B9-Vk15 and includes			
CC	the amino acid sequence beyond the first stop codon. The clone is			
CC	incomplete, starting from the G of the Arg initiator codon, but the			
CC	initial Met is given. Antibody molecules of the invention can			
CC	include one or two aberrant light chains containing a duplicated			

CC variable region, to produce heavier antibodies. These heavier
 CC antibodies were found to have higher avidity than antibodies with
 CC just a single copy of the L/V region. The antibodies can be used to
 CC treat disease, e.g. infection by Streptococcus agalactiae. They are
 CC able to pass across the placenta.
 CC See also Q11879 and Q11880.
 SQ Sequence 349 AA;

Query Match 83.5%; Score 513.5; DB 1; Length 349;
 Best Local Similarity 85.5%; Pred. No. 2,6e-31;
 Matches 100; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

OY 1 LWPDTGELVMTQSPATLSVSPGERATLSCRASSQSVSNLAWYQOKPGQAPRLITYGAS 60
 DB 13 LWPDTGELVMTQSPATLSVSPGERATLSCRASSQSVSNLAWYQOKPGQAPRLITYGAS 72
 OY 61 TRATGIPARFSGSGSTEFTLTISLQSEDFAVYYCCQYNNMPP-YTFGCGTKLEIK 116
 DB 73 NRATGIPARFSGSGSTEFTLTISLQSEDFAVYYCCQYNNMPPGATFGGCKVEIK 129

RESULT 5
 ID R13018
 AC R13018
 DT 01-AUG-1991 (first entry)
 DE 1B1 IgG aberrant light chain with duplicated variable region.
 KW Immunoglobulin G; light chain; variable region; duplication;
 OS Homo sapiens.
 FH Key location/Qualifiers
 FT peptide 1..17
 FT /label= leader peptide
 FT region 18..130
 FT /label= variable region
 FT /note= "L/V 1"
 FT region 131..243
 FT /label= variable region
 FT /note= "L/V 2"
 FT region 244..345
 FT /label= constant region

MO9106305-A.
 PD 16-MAY-1991.
 PR 06-NOV-1990; U06426.
 PR 07-NOV-1989; US-432700.
 PI (BRIM) BRISTOL-MYERS SQUIB.
 PI Shuford MW, Harris LJ, Raff HV;
 WP1: 91-163947/22.
 DR N-PDB: Q11878.

PT Oligomeric Immunoglobulin(s) with high avidity for antigen(s) -
 PT formed by duplicating esp. variable region of light chain of IgG
 PT Class
 PS Example 5; Fig 16; 104pp; English.
 CC This sequence is deduced from the cDNA clone 489-VK15 and includes
 CC the amino acid sequence beyond the first stop codon ("x" in the
 CC sequence represents a nonsense codon). The clone is incomplete,
 CC starting from the G of the ATG initiator codon, but the initial Met
 CC is given. Antibody molecules of the invention can include one or two
 CC aberrant light chains containing a duplicated variable region, to
 CC produce heavier antibodies. These heavier antibodies were found to
 CC have higher avidity than antibodies with just a single copy of the
 CC L/V region. The antibodies can be used to treat disease, e.g.
 CC infection by Streptococcus agalactiae. They are able to pass across
 CC the placenta.
 CC See also Q11879 and Q11880.
 SQ Sequence 414 AA;

Query Match 83.5%; Score 513.5; DB 1; Length 414;
 Best Local Similarity 85.5%; Pred. No. 3e-31;
 Matches 100; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

OY 1 LWPDTGELVMTQSPATLSVSPGERATLSCRASSQSVSNLAWYQOKPGQAPRLITYGAS 60
 DB 13 LWPDTGELVMTQSPATLSVSPGERATLSCRASSQSVSNLAWYQOKPGQAPRLITYGAS 72
 OY 61 TRATGIPARFSGSGSTEFTLTISLQSEDFAVYYCCQYNNMPP-YTFGCGTKLEIK 116
 DB 73 NRATGIPARFSGSGSTEFTLTISLQSEDFAVYYCCQYNNMPPGATFGGCKVEIK 129

RESULT 6
 ID R13111
 AC R13111
 DT 10-MAR-1993 (revised)
 DT 01-AUG-1991 (first entry)
 DE 1B1 IgG aberrant light chain with duplicated variable region.
 KW Immunoglobulin G; light chain; variable region; duplication;
 OS Homo sapiens.
 FH Key location/Qualifiers
 FT peptide 1..17
 FT /label= leader peptide
 FT region 18..130
 FT /label= variable region
 FT /note= "L/V 1"
 FT region 131..243
 FT /label= variable region
 FT /note= "L/V 2"
 FT region 244..345
 FT /label= constant region

MO9106305-A.
 PD 16-MAY-1991.
 PR 06-NOV-1990; U06426.
 PR 07-NOV-1989; US-432700.
 PI (BRIM) BRISTOL-MYERS SQUIB.
 PI Shuford MW, Harris LJ, Raff HV;
 WP1: 91-163947/22.
 DR N-PDB: Q11878.

PT Oligomeric Immunoglobulin(s) with high avidity for antigen(s) -
 PT formed by duplicating esp. variable region of light chain of IgG
 PT Class
 PS Example 5; Fig 16; 104pp; English.
 CC This sequence is deduced from the cDNA clone 489-VK15 and includes
 CC the amino acid sequence beyond the first stop codon ("x" in the
 CC sequence represents a nonsense codon). The clone is incomplete,
 CC starting from the G of the ATG initiator codon, but the initial Met
 CC is given. Antibody molecules of the invention can include one or two
 CC aberrant light chains containing a duplicated variable region, to
 CC produce heavier antibodies. These heavier antibodies were found to
 CC have higher avidity than antibodies with just a single copy of the
 CC L/V region. The antibodies can be used to treat disease, e.g.
 CC infection by Streptococcus agalactiae. They are able to pass across
 CC the placenta.
 CC See also Q11879 and Q11880.
 SQ Sequence 414 AA;

Query Match 83.5%; Score 513.5; DB 1; Length 414;
 Best Local Similarity 85.5%; Pred. No. 3e-31;
 Matches 100; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

OY 1 LWPDTGELVMTQSPATLSVSPGERATLSCRASSQSVSNLAWYQOKPGQAPRLITYGAS 60
 DB 13 LWPDTGELVMTQSPATLSVSPGERATLSCRASSQSVSNLAWYQOKPGQAPRLITYGAS 72
 OY 61 TRATGIPARFSGSGSTEFTLTISLQSEDFAVYYCCQYNNMPP-YTFGCGTKLEIK 116
 DB 73 NRATGIPARFSGSGSTEFTLTISLQSEDFAVYYCCQYNNMPPGATFGGCKVEIK 129

RESULT 7
 ID Y06842
 ID Y06842 standard; Protein: 214 AA.

AC Y06842;
DT 25-JUN-1999 (first entry)
Seq ID No:10 of JP11089576.
KW AntiHbs: monoclonal antibody; Epstein Barr virus; EBV; adr type;
KW human; Hbs antigen; hepatitis C.
OS Homo sapiens.
PN J11089576-A.
PD 06-APR-1999.
PF 19-SEP-1997: 255705.
PR 19-SEP-1997: JP-255705.
RA (NRSN.) NISSHINBO IND INC.
DR WPI: 99-281053/24.
DR N-PSDB: X32826.
PT Anti-Hbs monoclonal antibody - produced without the risk of Epstein
PT Barr virus contamination
PS Disclosure: Page 9-10; 12pp; Japanese.
CC The invention relates to an antiHbs monoclonal antibody having the
CC following properties: (A) CDR-3 of H chain variable region; (B) it
CC contains no Epstein Barr virus (EBV); (C) it binds at least one adr type
CC among human Hbs antigens. The antiHbs monoclonal antibody is high in
CC antibody titer and has low risk of EBV contamination. It can be used to
CC prevent hepatitis C.
SQ Sequence 214 AA;

Query Match 82.8%; Score 509.5; DB 1; Length 214;
Best Local Similarity 93.6%; Pred. No. 3.2e-31;
Matches 102; Conservative 1; Mismatches 5; Indels 1; Gaps 1;
OY 9 EIVMTQSPATISVSPGERATLSCRASQSVSSNLTANYQKPGQAPRLIYGA
DB 1 EIVMTQSPATISVSPGERATLSCRASQSVSSNLTANYQKPGQAPRLIYGA
OY 69 RFSGSGSTFEFTLTISLSQSEDFAVYCCQYNNMPYFGGCKLEIKR 117
DB 61 RFSGSGSTFEFTLTISLSQSEDFAVYCCQYNNMPYFGGCKLEIKR 108

RESULT 8
W11155
ID W11155 standard; Protein; 134 AA.
AC W11155;
DT 14-MAY-1997 (first entry)
DE Anti-lung tumour antigen monoclonal antibody light chain.
KW Light chain monoclonal; antibody; TB2A36C3; lung; tumour; EBV;
KW Epstein-Barr virus; TB945; human; B cell; screen; antigen;
KW carcinoma; lysis; anti-tumour therapy; activation; CD4; CD8;
KW B-cell.
OS Homo sapiens.
PN WO9628473-A1.
PD 19-SEP-1996.
PF 18-MAR-1996: U03661.
PR 16-MAR-1995: US-405034.
RA (MEDA.) MEDENICA R D.
PI Mukerjee S; 3664/43.
DR WPI: 96-433764/43.
DR N-PSDB: T33664.
PT Anti-lung tumour antigen monoclonal antibody TB2A36C3 - produced by
PT Epstein-Barr virus transformation of human lung cancer patient
PT B-cells, useful in conjunction with other agents for lysis of
PT tumours.
PS Claim 12; Page 25; 46pp; English.
CC The present sequence is the light chain from the monoclonal
CC antibody (Mab) TB2A36C3, which has high specificity against lung
CC tumour antigens and is produced by an Epstein-Barr virus (EBV)
CC transformed TB945 human B cell line. The Mab can be used to screen
CC serum or tissue samples for a carcinoma associated antigen, lyse
CC tumours in anti-tumour therapy (optionally with other agents) and
CC activate immune competent CD4 or CD8 cells in a patient's blood
CC system.
CC Tumour draining lymph nodes obtained from a non-SCLC (small cell
CC lung cancer) patient were cut into fine pieces and mashed. Pure B
CC cells, isolated using CD19 coated immunomagnetic beads, were

CC immortalised by EBV transformation, and plated and assayed for
CC activity. Clones which showed positive reactivity with autologous
CC tumour cells from the patient and the SCLC cell line NC1H69, were
CC subjected to limiting dilution to prepare the Mab.
SQ Sequence 134 AA;

Query Match 82.0%; Score 504.5; DB 1; Length 134;
Best Local Similarity 84.7%; Pred. No. 4.8e-31;
Matches 100; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

OY 1 LMLPDTGEIYMTQSPATISVSPGERATLSCRASQSVSSNLTANYQKPGQAPRLIYGA 59
DB 13 LMLPDTGEIYMTQSPATISVSPGERATLSCRASQSVSSNLTANYQKPGQAPRLIYGA 72
OY 60 STRATGIPDRFSGSGSTFEFTLTISLSQSEDFAVYCCQYNNMPYFGGCKLEIKR 117
DB 73 STRATGIPDRFSGSGSTFEFTLTISLSQSEDFAVYCCQYNNMPYFGGCKLEIKR 130

RESULT 9
R41286
ID R41286 standard; Protein; 129 AA.
AC R41286;
DT 01-NOV-1993 (first entry)
DE F105 rearranged variable region light chain.
KW Monoclonal antibody; Mab; envelope; glycoprotein; gp120; HIV; AIDS;
KW CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;
KW chain; epitope; immune deficiency.
OS Homo sapiens.
FH Key
FT peptide
FT 1.19
FT location/Qualifiers
FT /label-sig-peptide
FT 20.129
FT /label-mat-protein
PN WO9312232-A.
PD 24-JUN-1993.
PF 10-DEC-1992: U10928.
PR 10-DEC-1991: US-804652.
PA (DAND.) DANA FARBER CANCER INST INC.
PI (NEWB.) NEW ENGLAND DEACONNESS HOSPITAL CORP.
PI Haseltine WA; Marasco WA; Posner MR; Sodroski JG;
DR WPI: 93-214174/26.
DR N-PSDB: Q49155.
PT DNA segments encoding monoclonal antibody - which binds to gp120
PT and neutralises HIV, for treating AIDS, and for diagnosing and
PT monitoring HIV infection
PS Claim 10; Page 79; 109pp; English.
CC mRNA from the known hybridoma F105 was converted to cDNA and this
CC subjected to PCR amplification using primers corresp. to appropriate
CC parts of the heavy or light chains and having restriction sites to
CC permit cloning. The extension products were isolated and sequenced.
CC The recombinant human monoclonal antibody (Mab) binds to a
CC discontinuous epitope on the HIV gp120 envelope glycoprotein, blocks
CC the binding of gp120 to the CD4 receptor, and neutralises a broad
CC range of HIV isolates. The Mab may be used to treat immune
CC deficiency, esp. at doses of 0.1-10 mg/kg.
SQ Sequence 129 AA;

Query Match 81.1%; Score 499; DB 1; Length 129;
Best Local Similarity 84.7%; Pred. No. 1.2e-30;
Matches 100; Conservative 7; Mismatches 9; Indels 2; Gaps 2;

OY 1 LMLPDTGEIYMTQSPATISVSPGERATLSCRASQSVSSNLTANYQKPGQAPRLIYGA 59
DB 13 LMLPDTGEIYMTQSPATISVSPGERATLSCRASQSVSSNLTANYQKPGQAPRLIYGA 72
OY 60 STRATGIPDRFSGSGSTFEFTLTISLSQSEDFAVYCCQYNNMPYFGGCKLEIKR 117
DB 73 STRATGIPDRFSGSGSTFEFTLTISLSQSEDFAVYCCQYNNMPYFGGCKLEIKR 129

DR WPI: 91-163947/22.
 DR N-PSDB: Q11879.
 PT Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
 PT formed by duplicating esp. variable region of light chain of IgG
 PT class
 PS Example 4; Fig 17; 104pp; English.
 CC This sequence is derived from the nucleotide sequence encoding the
 CC light chain variable region. The "x" residues represent nonsense
 CC codons. The coding sequence has been translated in all 3 reading
 CC frames (see also R12130 and R12131). The L/V region is duplicated
 CC in so-called "aberrant" light chains (see Q11878), conferring
 CC increased avidity on antibodies comprising such aberrant chains.
 CC See also Q11880.
 SO Sequence 401 AA;

Query Match 80.2%; Score 493.5; DB 1; Length 401;
 Best Local Similarity 83.6%; Pred. No. 8.8e-30;

Matches 97; Conservative 7; Mismatches 11; Indels 1; Gaps 1;

OY 3 LPTDTGEIYVWTSPTATLSVSPGERATLSCRASQSVSNLAWYQKQKQAPRLIYGASR 62
 DB 221 ISDTTGEIYVWTSPTATLSVSPGERATLSCRASQSVSNLAWYQKQKQAPRLIYDASR 280
 OY 63 ATGIPARFSGSGGTFTLTISLSEDFAVYVYCCQYNNMPP-YTGGQTKLEIKR 117
 DB 281 ATGIPARFSGSGGTFTLTISLSEDFAVYVYCCQYNNMPPGATGTGKVEIKR 336

RESULT 13

W08946
 ID W08946 standard; Protein: 127 AA.

AC W08946;
 DT 18-SEP-1997 (first entry)
 DE Kappa light chain variable region of 225RA antibody.
 KM Kappa; light chain; reshaped; monoclonal; antibody; 225RA;
 KM human; epidermal growth factor; EGF; receptor; inhibition; growth;
 KM tumour; cell; late stage; prostatic; prostate; variable region.
 OS Homo sapiens.
 PN W09640210-A1.
 PD 19-DEC-1996.
 PF 07-JUN-1996; U09847.
 PR 07-JUN-1995; US-482982.
 PR 15-DEC-1995; US-573289.
 PA (IMCL-) IMCLONE SYSTEMS INC.
 PA (MRC-) MRC COLLABORATIVE CENT.
 PI Giorgio N. Goldstein NI, Jones ST, Saldanha JW.
 DR WPI: 91-051897/05.
 DR N-PSDB: T49345.
 PT Chimeric and humanised versions of anti-EGF receptor antibody 225 -
 PT used for inhibiting tumour growth, esp. of late stage prostatic
 PT tumour
 PS Claim 31; Fig 19; 112pp; English.
 CC The present sequence is the kappa light chain variable region
 CC of the reshaped human monoclonal antibody (MAb) H225, 225RA. The
 CC MAb is specific for the human epidermal growth factor (EGF)
 CC receptor.
 CC The MAb, or a fragment, can be used to inhibit the growth of tumour
 CC cells, especially late stage prostatic tumour cells in humans,
 CC optionally conjugated to a cytotoxic agent, especially doxorubicin,
 CC taxol or cisplatin, or a signal transduction, ras or cell cycle
 CC inhibitor.
 SO Sequence 127 AA;

Query Match 79.8%; Score 490.5; DB 1; Length 127;
 Best Local Similarity 81.0%; Pred. No. 5e-30;

Matches 94; Conservative 10; Mismatches 11; Indels 1; Gaps 1;

OY 1 LMLPDTGEIYVWTSPTATLSVSPGERATLSCRASQSVSNLAWYQKQKQAPRLIYGAS 60
 DB 13 LMLPDTGEIYVWTSPTATLSVSPGERATLSCRASQSVSNLAWYQKQKQAPRLIYKAS 72

OY 61 TRATGIPARFSGSGGTFTLTISLSEDFAVYVYCCQYNNMPPYTFGGTVEIKR 116
 DB 73 ESISGIPARFSGSGGTFTLTISLSEDFAVYVYCCQYNNMPPYTFGGTVEIKR 127

RESULT 14

R38648
 ID R38648 standard; Protein: 115 AA.

AC R38648;
 DT 10-NOV-1993 (first entry)
 DE Human V-kappa fragment encoded by clone vk05.3.
 KM Immunoglobulin; light chain variable region; minilocus;
 KM isotype switching; unrearranged functional V_K gene segment;
 KM human light chain transgene.
 OS Homo sapiens.
 PN W09312227-A.
 PD 24-JUN-1993.
 PF 17-DEC-1992; U10983.
 PR 17-DEC-1991; US-810279.
 PR 18-MAR-1992; US-853408.
 PR 23-JUN-1992; US-904068.
 PA (GENP-) GENPHARM INT INC.
 PI Kay RM, Londerg N.
 DR WPI: 93-214169/26.
 DR N-PSDB: Q44222.
 PT Transgenic non-human animals contg. immunoglobulin heavy chain
 PT trans gene - used to produce useful antibodies by isotype
 PT switching
 PS Example 21; Fig 41; 196pp; English.
 CC The V-kappa specific oligonucleotide Q50327 was used to probe a
 CC human placental genomic DNA library cloned into lambdaEMBL3/Sp6/T7.
 CC DNA fragments containing V-kappa segments from positive phage
 CC clones were subcloned into plasmid vectors. Variable gene segments
 CC from the resulting clones were sequenced and functional clones were
 CC selected on the basis of open reading frames, intact donor and
 CC acceptor splice sites and intact recombination sequences. The
 CC sequences obtained from four different plasmid clones were
 CC designated p65.3, p65.5, p65.8 and p65.15 (see Q44222-Q44225,
 CC respectively) and the amino acid sequences of the V-kappa regions
 CC they encode were deduced.
 SO Sequence 115 AA;

Query Match 79.5%; Score 489; DB 1; Length 115;
 Best Local Similarity 90.3%; Pred. No. 5.8e-30;
 Matches 93; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 LMLPDTGEIYVWTSPTATLSVSPGERATLSCRASQSVSNLAWYQKQKQAPRLIYGAS 60
 DB 13 LMLPDTGEIYVWTSPTATLSVSPGERATLSCRASQSVSNLAWYQKQKQAPRLIYDAS 72
 OY 61 TRATGIPARFSGSGGTFTLTISLSEDFAVYVYCCQYNNMPP 103
 DB 73 NRATGIPARFSGSGGTFTLTISLSEDFAVYVYCCQYNNMPP 115

RESULT 15

R62928
 ID R62928 standard; Protein: 115 AA.

AC R62928;
 DT 07-JUN-1995 (first entry)
 DE Human V-kappa vk65.3 region.
 KM Transgenic mouse; transgenic animal; antibody engineering;
 KM variable region; light chain; minilocus transgene;
 KM chimeric antibody.
 OS Homo sapiens.
 PN W09425585-A.
 PD 10-NOV-1994.
 PF 25-APR-1994; U04580.
 PR 26-APR-1993; US-053131.
 PR 22-JUL-1993; US-096762.
 PR 18-NOV-1993; US-135501.
 PR 03-DEC-1993; US-161739.

PR 10-DEC-1993; US-165699.
PR 09-MAR-1994; US-209741.
PA (GENP-) GENPHARM INT INC.
PI Kay RW, Londerg N;
DR WPI; 94-358263/44.
DR N-PSDB; Q78852.
PT Transgenic non-human animals producing heterologous or chimeric
PT antibodies - for binding a pre-determined human antigen with
PT increased affinity
PS Disclosure; Fig. 41; 296pp; English.
CC Human DNA fragments vk65.3, vk65.5, vk65.8 and vk65.15 (given in
CC Q78852-Q78855, respectively) each contain a V-kappa gene segment
CC that can be used to form a complete human light chain minilocus
CC transgene for expression in a nonhuman transgenic animal for
CC heterologous antibody production. The deduced amino acid
CC sequences of the V-kappa coding regions are given in R62928-R62931.
SQ Sequence 115 AA;

Query Match 79.5%; Score 489; DB 1; Length 115;
Best Local Similarity 90.3%; Pred. NO. 5.8e-30;
Matches 93; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY	1	LMLPDTGEIVMTQSPATLSVSPGERATLSCASQSVSNLAWYQKPGQAPRLIYGAS	60
DB	13	LMLPDTGEIVMTQSPATLSVSPGERATLSCASQSVSNLAWYQKPGQAPRLIYGAS	72
QY	61	TRATGIPARFSGSGGTFTLTISLQSEDFAVYYCOQNNMP	103
DB	73	NRATGIPARFSGSGGTFTLTISLQSEDFAVYYCOQNNMP	115

Search completed: July 26, 2000, 14:01:27
Job time: 2766 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 26, 2000, 14:21:22 ; Search time 43.23 seconds
(without alignments)
167.486 Million cell updates/sec

Title: US-09-203-768a-4

Perfect score: 615

Sequence: 1 LWLPDTGELVMTQSPATLS.....QYNNWPPYTFGGQTKLEIKR 117

Scoring table:

Gapop 10.0, Gapept 0.5

Search: 178050 seqs, 61884766 residues

Number of hits satisfying chosen parameters: 178050

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	588.5	95.7	128	2	S40343 Ig kappa chain V-J
2	574.5	93.4	117	2	S40362 Ig kappa chain - h
3	562	91.4	131	2	S40328 Ig kappa chain - h
4	539.5	87.7	123	2	S40378 Ig kappa chain - h
5	530.5	86.3	128	2	A56701 Ig kappa chain V r
6	527	85.7	115	1	K3HUC1 Ig kappa chain pre
7	526.5	85.6	107	2	S34005 Ig kappa chain V r
8	526	85.5	115	2	A30553 Ig kappa chain pre
9	525.5	85.4	144	2	PL0106 Ig kappa chain V-I
10	523	85.0	116	2	B26555 Ig kappa chain V-J
11	522	84.9	110	2	S40326 Ig kappa chain V-J
12	518.5	84.3	128	2	S40379 Ig kappa chain V-J
13	514	83.6	215	2	JE0244 Ig kappa chain V r
14	513.5	83.5	129	2	S29627 Ig kappa chain V r
15	511.5	83.2	114	2	S46375 Ig kappa chain V-J
16	510	82.9	129	1	K3HUA Ig kappa chain pre
17	510	82.9	129	2	S49532 anti-Sm antibody V
18	510	82.9	129	2	S46369 Ig kappa chain V r
19	510	82.9	134	2	S38643 Ig kappa chain V r
20	509.5	82.8	128	2	S40345 Ig kappa chain V-J
21	509	82.8	129	1	K3HUI Ig kappa chain pre
22	505	82.1	108	2	S40377 Ig kappa chain V-I
23	504	82.0	109	1	K3HUPM Ig kappa chain V-I
24	502	81.6	129	2	A32274 Ig kappa chain pre
25	498	81.1	128	2	S20636 Ig kappa chain V r
26	488	81.0	130	2	S20637 Ig kappa chain V r
27	466	80.7	114	2	S54905 Ig kappa chain V r
28	466	80.7	130	2	S40360 Ig kappa chain - h
29	494	80.3	129	2	S40363 Ig kappa chain - h

30	493.5	80.2	128	1	K3HUA1 Ig kappa chain pre
31	492.5	80.1	131	2	S40346 Ig kappa chain V-J
32	490.5	79.8	111	2	S33628 Ig kappa chain V r
33	489.5	79.6	125	2	S40344 Ig kappa chain V-J
34	489	79.5	115	1	K3HUVG Ig kappa chain pre
35	485.5	78.9	129	2	S40325 Ig kappa chain - h
36	485	78.9	121	2	S40327 Ig kappa chain - h
37	484	78.7	124	2	S20633 Ig kappa chain - h
38	482.5	78.5	215	2	UE0243 Ig kappa chain V r
39	479.5	78.0	119	2	S41816 Ig kappa chain V r
40	478	77.7	98	2	I30608 Ig kappa chain V-I
41	476	77.4	95	2	PH0868 Ig kappa chain V-I
42	475	77.2	109	2	H30601 Ig kappa chain V-I
43	471.5	76.7	108	2	G44151 Ig kappa chain V r
44	467	75.9	145	2	S20631 Ig kappa chain - h
45	465	75.6	108	2	C30608 Ig kappa chain V-I

ALIGNMENTS

RESULT 1
S40343
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40343
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chl genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40343
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-128 <KLE>
A:Cross-References: EMBL:X72453; NID:g441374; PIDN:CA651121.1; PID:g441375
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: Immunoglobulin homology <IMM>

Query Match 95.7%; Score 588.5; DB 2; Length 128;
Best Local Similarity 97.4%; Pred. No. 3.8e+42;
Matches 114; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
QY 1 LWLPDTGELVMTQSPATLSVSGERATLSRASQSVSSNTLAWYQKPGQAPRLIYGAS 60
|||||
DB 13 LWLPDTGELVMTQSPATLSVSGERATLSRASQSVSSNTLAWYQKPGQAPRLIYGAS 72
QY 61 TRATGTPARFSGSGSTETFLTISSLSQSEDFAVYCCQYNNWPPYTFGGQTKLEIKR 117
|||||
DB 73 TRATGTPARFSGSGSTETFLTISSLSQSEDFAVYCCQYNNWPPYTFGGQTKLEIKR 128
RESULT 2
S40362
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40362
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chl genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40362
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-111 <KLE>
A:Cross-References: EMBL:X72472; NID:g441412; PID:g441413
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:26-100/Domain: Immunoglobulin homology <IMM>

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Query Match similarity      93.4%: Score 574.5; DB 2; Length 117;
Best Local Similarity     96.6%: Pred. No. 4e-41;
Matches 112; Conservative 1; Mismatches 2; Indels 1; Gaps 1

OY   1 LMLPDTGTGIWVTOGPATLTVSPGEGRATLTSCRASQSVSSNLMAYOOQKPGCAPRLLIYGAS 60
DB   3 LMLPDTGTGIWVTOGPATLTVSPGEGRATLTSCRASQSVSSNLMAYOOQKPGCAPRLLIYGAS 62
OY   61 TRATGIPAFSGSGSCTEFTLTITSSIQSDFAFYVCQQYNMPPYTFGGGTKEIK 116
DB   63 TRATGIPAFSGSGSCTEFTLTITSSIQSDFAFYVCQQYNMNM-PLTFFGGGTKEIK 117

RESULT      3
SA40328
ig kappa chain - human
C:Species: Homo sapiens (man)
Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
Accession: S40328
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chl genes and their hypermutation.
A:Reference number: S40312; MID:9408091
A:Accession: S40328
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-131 <KLE>
C:Cross-references: EMBL.X72438; NID:g441344; PID:CAA51106.1; PID:g441345
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-109/Domain: immunoglobulin homology <IMM>

Query Match      91.4%: Score 562; DB 2; Length 131;
Best Local Similarity 89.7%: Pred. No. 5.9e-40;
Matches 105; Conservative 5; Mismatches 7; Indels 0; Gaps 0

OY   1 LMLPTGTGIWVTOGPATLTVSPGERATLTSCRASQSVSSNLMAYOOQKPGCAPRLLIYGAS 60
DB   12 LMLPTGTGVVMTGOSPATLTVSPGERATLTSCRASQSVHINLMAYOOQKPGCAPRLLIYGAV 71
OY   61 TRATGIPAFSGSGSCTEFTLTITSSIQSDFAFYVCQQYNMPPYTFGGGTKEIKR 117
DB   72 TRATGVPAFFSGSGSCTEFTLTITSSIQSDLTATYYCCQYNDMPWPFMGGTKEIKR 128

F.T.      4
SA40328
ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
Accession: S40328
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chl genes and their hypermutation.
A:Reference number: S40312; MID:9408091
A:Accession: S40328
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <KLE>
C:Cross-references: EMBL.X72488; NID:g441444; PID:CAA51156.1; PID:g441445
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:29-103/Domain: immunoglobulin homology <IMM>

Query Match      87.7%: Score 539.5; DB 2; Length 123;
Best Local Similarity 87.3%: Pred. No. 4e-36;
Matches 103; Conservative 6; Mismatches 8; Indels 1; Gaps 1

OY   1 LMLPTGTGIWVTOGPATLTVSPGERATLTSCRASQSVSSNLMAYOOQKPGCAPRLLIYGAS 60

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Db      6  IMLPGTGEIVYQTGPATLVSPPGDTALISCAASGVSSNLAWYQHRGQAPRLIIYCAS 65
OY      61  TMTATGPAPFSGSGSGCTEFTLTLSLQSEDFRAYVYCCQYNNMPP- YTGCGGKLEIKR 117
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      66  TPAAGTAPFSGSGSGCTEFTLTLSLQSEADFAIYVCCQYIDPMPTVYTGQGRILDIKR 123
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT  5
A56701
Ig kappa chain V region precursor (Hua) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000
C:Accession: A56701
R:Nickerson, K.G.; Tao, M.H.; Chen, H.T.; Larrick, J.; Kabat, E.A.
J. Biol. Chem. 270, 12457-12465, 1995
A:Title: Human and mouse monoclonal antipodles to blood group A substance, which are
A:Reference numbers: A56701, MUID:95279371
A:Accession: A56701
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-128 <NIC>
C:Cross-references: GB:I41174; NID:g762823; PID:AAA64877.1; PID:g762824
C:Superfamily: immunoglobulin V region: immunoglobulin homology
C:Keywords: heterotetramer, immunoglobulin
F:36-110/Domain: Immunoglobulin homology <IMM>

Query Match      86.3%; Score 530.5; DB 2; Length 128;
Best Local Similarity 88.0%; Pred. No. 2,3e-37;
Matches 103; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

OY      1  IMLPPTGEIVYQTGPATLVSPPGERATLSCRASQSVSSNLAWYQKFGQAPRLIIYCAS 60
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      13  IMLPPTGEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQKFGQAPRLIIYDAS 72
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

OY      61  TRATGTPAPFSGSGSGCTEFTLTLSLQSEDFRAYVYCCQYNNMPPYTGCGKLEIKR 117
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      73  NKAITGTPAPFSGSGSGCTEFTLTLSLQSEDFRAYVYCCQYNNM- PPSFGQKVEIKR 128
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT  6
K3HUC1
Ig kappa chain precursor V-III region (CLL) - human
N:Alternate names: rheumatoid factor
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 21-Jan-2000
C:Accession: A01898
R:Jirik, F.R.; Soergel, J.; Fong, S.; Heltzmann, J.G.; Curd, J.G.; Chen, P.P.; Goldfien
Proc. Natl. Acad. Sci. U.S.A. 83, 2195-2199, 1986
A:Title: Cloning and sequence determination of a human rheumatoid factor light-chain
A:Reference numbers: A01898, MUID:86177570
A:Accession: A01898
A:Molecule type: DNA
A:Residues: 1-115 <JIR>
A:Note: the sequence was determined from the germline gene
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
A:Inserts: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (L)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin V region: immunoglobulin homology
C:Keywords: autoantibody; chronic lymphocytic leukemia; heterotetramer; immunoglobulin
F:21-20/Domain: signal sequence #status predicted <SIG>
F:21-113/Product: rheumatoid factor, Ig kappa chain V-III region (CLL) #status predic
F:21-43/Region: framework 1
F:36-110/Domain: immunoglobulin homology <IMM>
F:55-69/Region: complementarity-determining 1
F:70-76/Region: complementarity-determining 2
F:77-108/Region: framework 3
F:109-115/Region: complementarity-determining 3

```


F:43-108/Disulfide bonds: #status predicted

Query Match 85.78; Score 527; DB 1; Length 115;

Best Local Similarity 97.18; Pred. No. 4,1e-37; Mismatches 2; Indels 0; Gaps 0;

Matches 100; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 13 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGAPRLIYGAS 60
13 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGAPRLIYGAS 72

RESULT 7

Ig kappa chain V region - human

C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S34005; S30524

R:Marlette, X.; Tsapis, A.; Brouet, J.C.

A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal

A:Reference number: S34001; MUID:93209281

A:Accession: S34005

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-107 <NAR>

A:Cross-references: EMBL:218330

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.68; Score 526.5; DB 2; Length 107;

Best Local Similarity 96.38; Pred. No. 4,2e-37; Mismatches 2; Indels 1; Gaps 1;

Matches 100; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Db 9 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGAPRLIYGAS 68
1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGAPRLIYGAS 60

RESULT 8

Ig kappa chain precursor V-III region (Hah) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000C:Accession: A30553
R:Ilju, M.F.; Robbins, D.L.; Crowley, J.J.; Sinha, S.; Kozin, F.; Kipps, T.J.; Carson, D.

A:Title: Characterization of four homologous L chain variable region genes that are rela

A:Reference number: A30553; MUID:89093959

A:Accession: A30553

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-115 <LUD>

A:Note: The sequence was determined from the differentiated gene

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 85.58; Score 526; DB 2; Length 115;

Best Local Similarity 97.18; Pred. No. 4,9e-37; Mismatches 2; Indels 0; Gaps 0;

Query Match 85.78; Score 527; DB 1; Length 115;

Best Local Similarity 97.18; Pred. No. 4,1e-37; Mismatches 2; Indels 0; Gaps 0;

Matches 100; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 13 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGAPRLIYGAS 60
13 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGAPRLIYGAS 72

Db 61 TRATGIPARFSGSGGTEFTLTISLSQSEDFAYVYCCQYNNMP 103

Db 73 TRATGIPARFSGSGGTEFTLTISLSQSEDFAYVYCCQYNNMP 115

RESULT 9

Ig kappa chain precursor V-J-C region (LS1) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000C:Accession: PLO106
R:Silberstein, L.E.; Litwin, S.; Carmack, C.E.

A:Title: Relationship of variable region genes expressed by a human B cell lymphoma s

A:Reference number: PLO106; MUID:89235583

A:Accession: PLO106

A:Molecule type: mRNA

A:Residues: 1-144 <STL>

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-115/Domain: V region <VRE>

F:36-110/Domain: immunoglobulin homology <IMM>

F:44-54/Region: complementarity-determining 1

F:70-76/Region: complementarity-determining 2

F:109-115/Region: complementarity-determining 3

F:116-127/Domain: J region <JRG>

F:128-144/Domain: C region (fragment) <CRE>

Query Match 85.48; Score 525.5; DB 2; Length 144;

Best Local Similarity 87.28; Pred. No. 6,7e-37; Mismatches 7; Indels 1; Gaps 1;

Matches 102; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

Db 13 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGAPRLIYGAS 60
13 LMLPDTGELVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGAPRLIYGAS 72

Db 61 TRATGIPARFSGSGGTEFTLTISLSQSEDFAYVYCCQYNNMP 117

Db 73 NRATGIPARFSGSGGTEFTLTISLSQSEDFAYVYCCQYNNMP 128

RESULT 10

Ig kappa chain V-III region (Ger) - human

C:Species: Homo sapiens (man)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000C:Accession: B26555
R:Midguth, C.R.; Litman, G.W.

A:Title: Atypical glycosylation of an IgG monoclonal cryoimmunoglobulin.

A:Reference number: A92630; MUID:87137666

A:Accession: B26555

A:Status: Preliminary

A:Molecule type: protein

A:Residues: 1-116 <MID>

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.08; Score 523; DB 2; Length 116;

Best Local Similarity 91.78; Pred. No. 8,8e-37; Mismatches 4; Indels 0; Gaps 0;

Matches 100; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Db 9 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGAPRLIYGAS 68
1 DIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQKPGAPRLIYGAS 60

OY 69 RFGSGSGTEFTLTISLQSEDFAYVYCCQYNNMPYTGQTKLEIKR 117
 DB 61 RFGSGSGTEFTLTISLQSEDFAYVYCCQYNNMPYTGQTKLEIKR 109

RESULT 11

IG kappa chain V-J region - human
 S40326
 C:Species: Homo sapiens (man)
 C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S40326
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A:Title: Expressed human immunoglobulin chl genes and their hypermutation.
 A:Reference number: S40312; MUID:94080891
 A:Accession: S40326
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-110 <KLB>
 A:Cross-References: EMBL:X72436
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:32-106/Domain: immunoglobulin homology <IMM>

Query Match 84.9%; Score 522; DB 2; Length 110;
 Best Local Similarity 100.0%; Pred. No. 1e-36;
 Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LMLPDTGEIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIYGAS 60
 DB 9 LMLPDTGEIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIYGAS 68
 OY 61 TRATGIPARFSSGSGTEFTLTISLQSEDFAYVYCCQYNN 101
 DB 69 TRATGIPARFSSGSGTEFTLTISLQSEDFAYVYCCQYNN 109

RESULT 12

IG kappa chain V-J region - human
 S40379
 C:Species: Homo sapiens (man)
 C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C:Accession: S40379
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.
 Eur. J. Immunol. 23, 3248-3271, 1993
 A:Title: Expressed human immunoglobulin chl genes and their hypermutation.
 A:Reference number: S40312; MUID:94080891
 A:Accession: S40379
 A:Status: preliminary; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-128 <KLB>
 A:Cross-References: EMBL:X72489; NID:g441446; PIDN:CA51157.1; PID:g441447
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 84.3%; Score 518.5; DB 2; Length 128;
 Best Local Similarity 85.5%; Pred. No. 2.3e-36;
 Matches 100; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

OY 1 LMLPDTGEIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIYGAS 60
 DB 13 LMLPDTGEIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIYGAS 72
 OY 61 TRATGIPARFSSGSGTEFTLTISLQSEDFAYVYCCQYNNMPYTGQTKLEIKR 117
 DB 73 NRATGIPARFSSGSGTEFTLTISLQSEDFAYVYCCQYNNMPYTGQTKLEIKR 128

RESULT 13

JE0244

IG kappa chain NIG2 precursor - human
 C:Species: Homo sapiens (man)
 C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
 C:Accession: JE0244
 R:Alim, M.A.; Hara, Y.; Hossein, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.
 submitted to JIPID, November 1998
 A:Description: A new subgroup of k type light chains (kV) identified in cases of AL
 A:Reference number: JE0243
 A:Accession: JE0244
 A:Molecule type: protein
 A:Residues: 1-215 <ALJ>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 83.6%; Score 514; DB 2; Length 215;
 Best Local Similarity 89.9%; Pred. No. 8.8e-36;
 Matches 98; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 9 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIYGASTRATGIPA 68
 DB 1 EIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIYRASTRATGIPA 60
 OY 69 RFGSGSGTEFTLTISLQSEDFAYVYCCQYNNMPYTGQTKLEIKR 117
 DB 61 RFGSGSGTEFTLTISLQSEDFAYVYCCQYNNMPYTGQTKLEIKR 109

RESULT 14

IG kappa chain V region (60.3 hybridoma) - human
 S29627
 C:Species: Homo sapiens (man)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
 C:Accession: S34110; S29627
 R:Walls, M.A.; Hsiao, K.; Harris, L.J.
 Nucleic Acids Res. 21, 2921-2929, 1993
 A:Title: Vectors for the expression of PCR-amplified immunoglobulin variable domains
 A:Reference number: S34110; MUID:93324379
 A:Accession: S34110
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-129 <MA2>
 A:Cross-References: EMBL:Z17330; NID:g48511; PIDN:CA78978.1; PID:g38512
 A>Note: human sequences cloned and sequenced prior to expression in mouse myeloma cell
 C:Genetics: 17/1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 83.5%; Score 513.5; DB 2; Length 129;
 Best Local Similarity 85.5%; Pred. No. 5.9e-36;
 Matches 100; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

OY 1 LMLPDTGEIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIYGAS 60
 DB 13 LMLPDTGEIVMTQSPATLSVSPGERATLSCRASQSVSNLAWYQOKPGQAPRLIYGAS 72
 OY 61 TRATGIPARFSSGSGTEFTLTISLQSEDFAYVYCCQYNNMPYTGQTKLEIKR 116
 DB 73 NRATGIPARFSSGSGTEFTLTISLQSEDFAYVYCCQYNNMPYTGQTKLEIKR 129

RESULT 15

IG kappa chain V-J region (733-5) - human (fragment)
 S46375
 C:Species: Homo sapiens (man)
 C>Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
 C:Accession: S46375; S38648
 R:Bensimon, C.; Chastagner, P.; Zouali, M.
 EMBO J. 13, 2951-2962, 1994

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Db 73 TRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

RESULT 2

ID KV3M.HUMAN STANDARD; PRT; 129 AA.

AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-II REGION HAH PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RN Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
[1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 88171307.

RK Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;

"Antibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
J. Exp. Med. 167:840-852(1988).

-1- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC LEUKEMIA.

DR PIR: P10022; K3HUA.

DR HSSP: P01789; 2MCP.

DR PFAM: PF00047; 19; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20

FT CHAIN 21 129 IG KAPPA CHAIN V-II REGION HAH.

FT DOMAIN 21 43 FRAMEWORK 1.

FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 56 70 FRAMEWORK 2.

FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 78 109 FRAMEWORK 3.

FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 119 129 JKL SEGMENT.

FT DISULFID 43 109 BY SIMILARITY.

FT NON TER 129 129

SO SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 82.9%; Score 510; DB 1; Length 129;

Best Local Similarity 85.6%; Pred. No. 4.7e-43;

Matches 101; Conservative 7; Mismatches 8; Indels 2; Gaps 2;

Db 13 LWPDTGELVMTQSPATLSVSPGERATLSCRASQSVSSN-LAWYQKPGQAPRLIYGA 59

Db 13 LWPDTGELVMTQSPATLSVSPGERATLSCRASQSVSSN-LAWYQKPGQAPRLIYGA 72

Db 60 STRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 117

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

RT expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";

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DR PIR: P10022; K3HUA.

DR HSSP: P01789; 2MCP.

DR PFAM: PF00047; 19; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20

FT CHAIN 21 129 IG KAPPA CHAIN V-II REGION HAH.

FT DOMAIN 21 43 FRAMEWORK 1.

FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.

FT DOMAIN 56 70 FRAMEWORK 2.

FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.

FT DOMAIN 78 109 FRAMEWORK 3.

FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING 3.

FT DOMAIN 119 129 JKL SEGMENT.

FT DISULFID 43 109 BY SIMILARITY.

FT NON TER 129 129

SO SEQUENCE 129 AA; 14070 MW; 7395528EA2B74D6 CRC64;

Query Match 82.8%; Score 509; DB 1; Length 129;

Best Local Similarity 84.7%; Pred. No. 5.9e-43;

Matches 100; Conservative 9; Mismatches 7; Indels 2; Gaps 2;

Db 13 LWPDTGELVMTQSPATLSVSPGERATLSCRASQSVSSN-LAWYQKPGQAPRLIYGA 59

Db 13 LWPDTGELVMTQSPATLSVSPGERATLSCRASQSVSSN-LAWYQKPGQAPRLIYGA 72

Db 60 STRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 117

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

Db 73 SSRATGIPARFSSGSGTEFTLITSLQSEDFAYVYCCQYNNMPWTGQGRVETIKR 129

OY 68 ARFGSSGTEFTLTISSLOSEDFAVYCCOQYNNMPPYFGGTLEIKR 117
 DB 61 ARFGSSGTEFTLTISSLOSEDFAVYCCOQYNNMPPYFGGTLEIKR 109

RESULT 5

KV3J_HUMAN STANDARD; PRT; 128 AA.

AC P06311;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-II REGION IARC/BL41 PRECURSOR.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

RN [1]
 RB SEQUENCE FROM N.A.
 RM MEDLINE; 86041852.

RT K10beck H.G., Melndi A., Combrato G., Solomon A., Zachau H.G.;
 RT "Human Immunoglobulin kappa light chain genes of subgroups II and III."

RL Nucleic Acids Res. 13:6499-6513(1985).

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CC EMBL; Z00021; CAA7316.1; -

DR PIR; A01899; K3H041.

DR PIR; P00047; 1g; 1.

KW Immunoglobulin V region; signal.

FT SIGNAL 1 20

FT CHAIN 21 128

FT DOMAIN 21 43

FT DOMAIN 44 54

FT DOMAIN 55 69

FT DOMAIN 70 76

FT DOMAIN 77 108

FT DOMAIN 109 117

FT DOMAIN 118 128

FT DISULFID 43 108

FT NON_TER 128 128

SEQUENCE 128 AA; 14070 MW; CC8957F0FE3B9012 CRC64;

Query Match 80.2%; Score 493.5; DB 1; Length 128;

Best Local Similarity 82.9%; Pred. No. 1.9e-41;

Matches 97; Conservative 7; Mismatches 12; Indels 1; Gaps 1;

OY 1 LMLPTTGEIYVTOGSPATLSVSPERATLSGRASQSVSSNLAWYQKRGAPRLIYGAS 60

DB 13 LMLPTTGEIYVTOGSPATLSVSPERATLSGRASQSVSSNLAWYQKRGAPRLIYGAS 72

OY 61 TRAGCIPARFSGSGTEFTLTISSLOSEDFAVYCCOQYNNMPPYFGGTLEIKR 117

DB 73 SRANGCIPARFSGSGTEFTLTISSLOSEDFAVYCCOQYNNMPPYFGGTLEIKR 128

RESULT 6

KV3J_HUMAN STANDARD; PRT; 115 AA.

AC P04433;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-II REGION VH PRECURSOR (FRAGMENT).
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

RN [1]
 RB SEQUENCE FROM N.A.

RM MEDLINE; 85087932.

RT Peck M., Zachau H.G.;

RT "Immunoglobulin genes of different subgroups are interdigitated within the V_H locus."

RL Nucleic Acids Res. 12:9229-9236(1984).

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CC EMBL; X01668; -; NOT_ANNOTATED_CDS.

DR PIR; A01900; K3H04G.

DR PIR; P00047; 1g; 1.

KW Immunoglobulin V region; signal.

FT SIGNAL 1 20

FT CHAIN 21 >115

FT DOMAIN 21 43

FT DOMAIN 44 54

FT DOMAIN 55 69

FT DOMAIN 70 76

FT DOMAIN 77 108

FT DOMAIN 109 115

FT DISULFID 43 108

FT NON_TER 115 115

SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;

Query Match 79.5%; Score 489; DB 1; Length 115;

Best Local Similarity 90.3%; Pred. No. 4.5e-41;

Matches 93; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

OY 1 LMLPTTGEIYVTOGSPATLSVSPERATLSGRASQSVSSNLAWYQKRGAPRLIYGAS 60

DB 13 LMLPTTGEIYVTOGSPATLSVSPERATLSGRASQSVSSNLAWYQKRGAPRLIYGAS 72

OY 61 TRAGCIPARFSGSGTEFTLTISSLOSEDFAVYCCOQYNNMPPYFGGTLEIKR 103

DB 73 NRAGCIPARFSGSGTEFTLTISSLOSEDFAVYCCOQYNNMPPYFGGTLEIKR 115

RESULT 7

KV3J_HUMAN STANDARD; PRT; 116 AA.

AC P04434;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-II REGION VH PRECURSOR (FRAGMENT).

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

RN [1]
 RB SEQUENCE FROM N.A.

RM MEDLINE; 85087932.

RT Peck M., Zachau H.G.;

RT "Immunoglobulin genes of different subgroups are interdigitated within the V_H locus."

RL Nucleic Acids Res. 12:9229-9236(1984).

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or send an email to license@slb.ch).

CC EMBL: X02725; -; NOT_ANNOTATED_CDS.
DR PIR: A01901; K3HUVH.
DR HSSP: P01789; 2MCP.
DR PFAM: PF00047; 19; 1.
KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20
FT CHAIN 21 >116 IG KAPPA CHAIN V-III REGION VH.
FT DOMAIN 21 43 FRAMEWORK 1. DETERMINING 1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 56 70 FRAMEWORK 2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 78 109 FRAMEWORK 3.
FT DOMAIN 110 116 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA: 12757 MW: 51CD55BA53B21929 CRC64;

Query Match 74.6%; Score 458.5; DB 1; Length 116;
Best Local Similarity 87.5%; Pred. No. 4.2e-38;
Matches 91; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

OY 1 LMLPDTGEIYVQSPATLSVSPGERATISCRASQSVSSN-LAMYQKPGQAPRLIYGA 59
DB 13 LMLPDTREIYVQSPATLSVSPGERATISCRASQSVSSN-LAMYQKPGQAPRLIYGA 72
OY 60 STRATGIPARFSGSGSTFTLTISLQSEDFAVYVCOQYNNMP 103
DB 73 STRATGIPARFSGSGSTFTLTISLQSEDFAVYVCOQYNNMP 116

RESULT 8

KV3B_HUMAN STANDARD; PRT; 109 AA.
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION SITE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE; 82046598.
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human Igm anti-gamma-globulins of the Wa
RT group".
RL Biochemistry 20:5816-5822(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR: A01892; K3HUSI.
DR HSSP: P01789; 2MCP.
DR PFAM: PF00047; 19; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89
FT NON_TER 109 109 BY SIMILARITY.
SQ SEQUENCE 109 AA: 11775 MW: 7689C3EC6D46FFB4 CRC64;

Query Match 73.8%; Score 454; DB 1; Length 109;
Best Local Similarity 82.7%; Pred. No. 1.1e-37;
Matches 91; Conservative 9; Mismatches 8; Indels 2; Gaps 2;

OY 9 EIVYVQSPATLSVSPGERATISCRASQSVSSN-LAMYQKPGQAPRLIYGA STRATGIP 67
DB 1 EIVYVQSPATLSVSPGERATISCRASQSVSSN-LAMYQKPGQAPRLIYGA STRATGIP 60
OY 68 ARFSGSGSTFTLTISLQSEDFAVYVCOQYNNMPYFGGTLEIKR 117

DB 61 DRFSGSGSTFTLTISLQSEDFAVYVCOQYXS-SPQFGGSKVEIKR 109

RESULT 9

KV3D_HUMAN STANDARD; PRT; 109 AA.
AC P01622;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION TI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE; 72188439.
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein
RT ti). IV. The complete amino acid sequence and its significance for
RT the mechanism of antibody production".
RL Hope-Seyler's Z. Physiol. Chem. 353:189-208(1972).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01895; K3HUTI.
DR HSSP: P01789; 2MCP.
DR PFAM: PF00047; 19; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 109 109
SQ SEQUENCE 109 AA: 11788 MW: 8C35058CC07749BC CRC64;

Query Match 73.0%; Score 449; DB 1; Length 109;
Best Local Similarity 81.8%; Pred. No. 3.3e-37;
Matches 90; Conservative 10; Mismatches 8; Indels 2; Gaps 2;

OY 9 EIVYVQSPATLSVSPGERATISCRASQSVSSN-LAMYQKPGQAPRLIYGA STRATGIP 67
DB 1 EIVYVQSPATLSVSPGERATISCRASQSVSSN-LAMYQKPGQAPRLIYGA STRATGIP 60
OY 68 ARFSGSGSTFTLTISLQSEDFAVYVCOQYNNMPYFGGTLEIKR 117
DB 61 DRFSGSGSTFTLTISLQSEDFAVYVCOQYXS-SPQFGGSKVEIKR 109

RESULT 10

KV3E_HUMAN STANDARD; PRT; 109 AA.
AC P01623;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION WOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE; 82046598.
RA Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human Igm anti-gamma-globulins of the Wa
RT group".
RL Biochemistry 20:5816-5822(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR: A01896; K3HUTL.
DR HSSP: P01789; 2MCP.
DR PFAM: PF00047; 19; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.

FT NON_TER 109 109
SQ SEQUENCE 109 AA: 11746 MW: 566C115E6B9CBECE CRC64;

Query Match 72.8%; Score 448; DB 1; Length 109;
Best Local Similarity 82.7%; Pred. No. 4, 1e-37;
Matches 91; Conservative 7; Mismatches 10; Indels 2; Gaps 2;

OY 9 EIVMTQSPATLSVSPGERATLSCRASQSVSN-LAWYQOKPGQAPRLIYGASTRATGIP 67
DB 1 EIVLQSPPTLSLSPGERATLSCRASQSVSGTIGWYQOKPGQAPRLIYGASTRATGIP 60

OY 68 ARFSGSGSTFTLTISLQSEDFAVYVCOQYNNMPYFGQGTKEIKR 117
DB 61 DRFSGSGSTFTLTISRLPEDFAVYVCOQYGS-LGRFGQGTKEIKR 109

RESULT 11
KV3A_HUMAN STANDARD: PRT: 108 AA.
P01619:

DI 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION B6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RN Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RP SEQUENCE.
RA Milstein C.;
RT "The basic sequences of immunoglobulin kappa chains: sequence studies
of Bence Jones proteins Rad. Fz4 and B6.";
RL FEBS Lett. 2:301-304(1969).
CC -1- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.
DR HSSP; P01789; 2MCP.
DR PFAM; PF00047; 19; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 23 89 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA: 11635 MW: 8BC14FE07A419E3D CRC64;

Query Match 71.5%; Score 440; DB 1; Length 108;
Best Local Similarity 77.1%; Pred. No. 2, 4e-36;
Matches 84; Conservative 13; Mismatches 10; Indels 2; Gaps 2;

OY 9 EIVMTQSPATLSVSPGERATLSCRASQSVSN-LAWYQOKPGQAPRLIYGASTRATGIP 67
DB 1 ZIVLTSPTLSLSPGERATLSCRASQSVSGTIGWYQOKPGQAPRLIYGASTRATGIP 60

OY 68 ARFSGSGSTFTLTISLQSEDFAVYVCOQYNNMPYFGQGTKEIKR 116
DB 61 DRFSGSGSTFTLTISRLPEDFAVYVCOQYGS-SPTFGQGTKEIKR 108

RESULT 12
KV1M_HUMAN STANDARD: PRT: 108 AA.
P01605:

DI 21-JUL-1986 (rel. 01, Created)
DT 21-JUL-1986 (rel. 01, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION IAY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RN Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RP SEQUENCE.
RA MEDLINE; 77038198.
RA Capra J.D., Klapper D.G.;
KW "Complete amino acid sequence of the variable domains of two human

RT Igm anti-gamma globulins (Iay/Pom) with shared idiotypic
RT specificities.";
RL Scand. J. Immunol. 5:677-684(1976).

CC -1- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A01871; KIHITX.
DR HSSP; P01607; IRET.
DR PFAM; PF00047; 19; 1.

KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA: 11834 MW: 73993A95431434A CRC64;

Query Match 70.8%; Score 435.5; DB 1; Length 108;
Best Local Similarity 73.4%; Pred. No. 6, 7e-36;
Matches 80; Conservative 16; Mismatches 12; Indels 1; Gaps 1;

OY 9 EIVMTQSPATLSVSPGERATLSCRASQSVSN-LAWYQOKPGQAPRLIYGASTRATGIP 68
DB 1 DIQMTQSPATLSVSPGERATLSCRASQSVSGTIGWYQOKPGQAPRLIYGASTRATGIP 60

OY 69 ARFSGSGSTFTLTISLQSEDFAVYVCOQYNNMPYFGQGTKEIKR 117
DB 61 DRFSGSGSTFTLTISRLPEDFAVYVCOQYNNMPYFGQGTKEIKR 108

RESULT 13
KV4C_HUMAN STANDARD: PRT: 134 AA.
P06314:

DI 01-JAN-1988 (rel. 06, Created)
DT 01-APR-1988 (rel. 07, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-IV REGION B17 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
RN Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RP SEQUENCE FROM N.A.
RA MEDLINE; 86041854.
RA Marsh P., Mills F., Gould H.;
RT "Detection of a unique human V kappa IV germline gene by a cloned
RT cDNA probe.";
RL Nucleic Acids Res. 13:6531-6544(1985).

RN [2]
RP REVISION TO 76.
RA Marsh P.;
RL Submitted (OCT-1986) to the EMBL/Genbank/DBJ databases.

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DR EMBL; X02990; GA26733.1; -
DR PIR; A01905; K4HUI7.
DR HSSP; P01789; 2MCP.
DR PFAM; PF00047; 19; 1.
KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20
FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 61 75 FRAMEWORK 2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 83 114 FRAMEWORK 3.
FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 122 133 FRAMEWORK 4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 134 134
SQ SEQUENCE 134 AA; 14966 MW; 6413A22ED0738832 CRC64;

Query Match 69.88; Score 429.5; DB 1; Length 134;
Best Local Similarity 69.98; Pred. No. 3.3e-35;
Matches 86; Conservative 16; Mismatches 14; Indels 7; Gaps 3;

1 LMDPTTGEIYMTOSPATISVSGERATLSCRASQSV--SSN---LAWYQKPGQAPRL 54
13 LMSGAYGDIYMTOSPSLAVSLGERATLNCKSSQSLIYSSDNKNYLAWYQKPGQAPRL 72
DB 13 LMSGAYGDIYMTOSPSLAVSLGERATLNCKSSQSLIYSSDNKNYLAWYQKPGQAPRL 72
QY 55 LIYGASTRATGIPARFSGSGSGTEFTLTISLSQSEDAVYVCOQYNNMPYTFGQGTLE 114
DB 73 LIYASTRESGVDPREFSGSGSGTEFTLTISLSQSEDAVYVCOQYNNMPYTFGQGTLE 131
QY 115 IKR 117
DB 132 IKR 134

RESULT 14
KV3G_HUMAN
ID KV3G_HUMAN STANDARD; PRT; 109 AA.
AC P04206; 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION GOL (RHEUMATOID FACTOR).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP MEDLINE; 86230578.
RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
"Amino acid sequence of a light chain variable region of a human
rheumatoid factor of the Wa idiotype group, in part predicted by its
reactivity with anti-peptide antibodies.";
RL Mol. Immunol. 23:239-244(1986).
DR PIR: A01893; K3HUGO.
DR HSSP: P01789; 2MCP.
DR PRAM: PF00047; 19; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89
FT NON_TER 109 109 BY SIMILARITY.
SQ SEQUENCE 109 AA; 11830 MW; 9349A5BD93588B6 CRC64;

Query Match 69.68; Score 428; DB 1; Length 109;
Best Local Similarity 78.28; Pred. No. 3.6e-35;
Matches 86; Conservative 10; Mismatches 12; Indels 2; Gaps 2;

QY 9 EIVMTOSPATISVSGERATLSCRAS--OSVSNLAWYQKPGQAPRLIYASTRATGIP 67
DB 1 EIVMTOSPATISVSGERATLSCRAS--OSVSNLAWYQKPGQAPRLIYASTRATGIP 60
QY 68 ARFSGSGSGTEFTLTISLSQSEDAVYVCOQYNNMPYTFGQGTLEIKR 117
DB 61 DRFSGSGSGTEFTLTISLSQSEDAVYVCOQYNNMPYTFGQGTLEIKR 109
RESULT 15

KV4B_HUMAN
ID KV4B_HUMAN STANDARD; PRT; 133 AA.
AC P06313; 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-IV REGION JI PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86041853.
RA Klobbeck H.G., Bornkamm G.W., Combrato G., Mocikat R., Pohlentz H.D.,
Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
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CC EMBL; Z00022; CAA77317.1; --
DR PIR: A01904; K4HUII.
DR HSSP: P01789; 2MCP.
DR PRAM: PF00047; 19; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 IG KAPPA CHAIN V-IV REGION JI.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 61 75 FRAMEWORK 2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 83 114 FRAMEWORK 3.
FT DOMAIN 115 122 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 123 132 FRAMEWORK 4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14632 MW; 5FB395306744AF4 CRC64;

Query Match 68.58; Score 421; DB 1; Length 133;
Best Local Similarity 69.98; Pred. No. 2.2e-34;
Matches 86; Conservative 15; Mismatches 14; Indels 8; Gaps 3;

QY 1 LMDPTTGEIYMTOSPATISVSGERATLSCRASQSV--SSN---LAWYQKPGQAPRL 54
DB 13 LMSGAYGDIYMTOSPSLAVSLGERATLNCKSSQSLIYSSDNKNYLAWYQKPGQAPRL 72
QY 55 LIYGASTRATGIPARFSGSGSGTEFTLTISLSQSEDAVYVCOQYNNMPYTFGQGTLE 114
DB 73 LIYASTRESGVDPREFSGSGSGTEFTLTISLSQSEDAVYVCOQYNNMPYTFGQGTLE 130
QY 115 IKR 117
DB 131 IKR 133

Search completed: July 26, 2000, 14:25:25
Job time: 1331 sec

Wed Jul 26 15:40:47 2000

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OM protein - protein search, using sw model

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(without alignments)
166.265 Million cell updates/sec

Title: US-09-203-768a-4
Perfect score: 615
Sequence: 1 LMLPDTGELVMTQSPATLS.....QYNNMPPTGEGTKLEIKR 117

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: SP-archaea:*
2: SP-bacteria:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	145	23.6	123	11	061243
2	123	20.0	235	6	09XSM6
3	120.5	19.6	210	6	P79336
4	120	19.5	147	4	Q9Y509
5	117.5	19.1	397	4	Q9Y4V0
6	117	19.0	503	4	P78324
7	115.5	18.8	398	4	000241
8	114	18.5	209	6	09XSM7
9	109.5	17.8	118	11	Q9Z1C4
10	108.5	17.6	136	13	Q9YHR9
11	108	17.6	100	6	Q9YHR9
12	107	17.4	150	4	Q9Y298
13	105.5	17.2	506	6	Q46631
14	105	17.1	228	11	Q70153
15	104	16.9	198	4	Q13970
16	103	16.7	700	4	Q75054
17	102.5	16.7	142	11	Q9YH02
18	102	16.6	113	13	P97797
19	101.5	16.5	136	13	Q9YHP2

20	100.5	16.3	140	13	Q9YHF9
21	99	16.1	2222	5	Q97394
22	98.5	16.0	122	4	Q99604
23	98.5	16.0	133	13	Q9YHHA
24	98.5	16.0	506	6	Q46632
25	97.5	15.9	122	4	Q99603
26	97.5	15.9	143	13	Q9YH07
27	97	15.8	100	13	Q9YH19
28	96.5	15.7	105	13	Q9YH10
29	96.5	15.7	136	13	Q9YHP4
30	96.5	15.7	318	13	Q9YH64
31	96	15.6	100	13	Q9YHJ1
32	96	15.6	138	13	Q9YHF7
33	96	15.6	142	13	Q9YHM3
34	96	15.6	157	4	Q95978
35	95.5	15.5	144	13	Q9YHK9
36	94.5	15.4	134	13	Q9YHF8
37	94.5	15.4	136	13	Q9YHP3
38	94.5	15.4	137	13	Q9YHS0
39	94	15.3	152	13	Q9YH00
40	93.5	15.2	138	13	Q9YH26
41	93.5	15.2	235	13	Q90770
42	93	15.1	97	4	Q43234
43	93	15.1	99	13	Q9YHM5
44	93	15.1	101	13	Q9YHJ6
45	93	15.1	131	13	Q9YH17

ALIGNMENTS

RESULT 1

ID	061243	PRELIMINARY:	PRT:	123 AA.
AC	061243:			
DT	01-NOV-1996 (TRENDELREL. 01, Created)			
DT	01-NOV-1996 (TRENDELREL. 01, Last sequence update)			
DT	01-NOV-1999 (TRENDELREL. 12, Last annotation update)			
DE	8HS20 PROTEIN PRECURSOR.			
GN	VPREB3..			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BALB/C;			
RC	MEDLINE: 93259124.			
RA	SHIRASAWA T., OHNISHI K., HAGIWARA S., SHIGEMOTO K., TAKEBE Y.,			
RA	RAJESWARY K., TAKEMORI T.;			
RT	"A novel gene product associated with mu chains in immature B cells."			
RL	EMBO J. 12:1827-1834(1993).			
DR	EMBL: D13208; BAA02495.1; ..			
DR	MGI: 98938; VPREB3.			
DR	PFAM: PF00047; 19; 1.			
FT	CHAIN			
FT	SEQUENCE 123 AA; 13400 MW; DA2A70D3 CRC32;			

8HS20 PROTEIN.

Query Match 23.6%; Score 145; DB 11; Length 123;
Best Local Similarity 40.2%; Pred. No. 6,46-08;
Matches 41; Conservative 13; Mismatches 38; Indels 10; Gaps 5;

QY	12	MTQSPATLSVSPGERATISCRASQSVSS---NLAWYQKRGQARRLITYGAST---RAT 64
DB <td>23 <td>LTQ-PDARVSPFGDPAHSLCTINSQHAATGAGISWYQOQPSAFLHYAAEEHYPRA 81 </td></td>	23 <td>LTQ-PDARVSPFGDPAHSLCTINSQHAATGAGISWYQOQPSAFLHYAAEEHYPRA 81 </td>	LTQ-PDARVSPFGDPAHSLCTINSQHAATGAGISWYQOQPSAFLHYAAEEHYPRA 81
QY <td>65 <td>GIPARFSGS--GSGTEFTLTSSLOSEDFAYVYCCQYNNMP 104</td> </td>	65 <td>GIPARFSGS--GSGTEFTLTSSLOSEDFAYVYCCQYNNMP 104</td>	GIPARFSGS--GSGTEFTLTSSLOSEDFAYVYCCQYNNMP 104
DB <td>82 <td>DIPDRFSATVDAAHNAACILITISPIVLPEDDADYFCISATIFEP 123</td> </td>	82 <td>DIPDRFSATVDAAHNAACILITISPIVLPEDDADYFCISATIFEP 123</td>	DIPDRFSATVDAAHNAACILITISPIVLPEDDADYFCISATIFEP 123

RESULT 2

Q9XSM6

ID 09XSM6 PRELIMINARY; PRT; 235 AA.
AC 09XSM6;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE CD8 ALPHA CHAIN PRECURSOR.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-92039;
RC MEDLINE; 99299362.
RA URETA-VIDAL A., GARCIA Z., LEMONNIER F.A., KAZANJI M.;
RT "Molecular characterization of cDNAs encoding squirrel monkey (Saimiri sciureus) CD8 alpha and beta chains";
RL Immunogenetics 49:718-721(1999).
DR EMBL; AJ130818; CAB41462.1; -.
FT SIGNAL.
FT CHAIN 1 21 POTENTIAL.
FT CHAIN 22 235 CD8 ALPHA CHAIN.
SQ SEQUENCE 235 AA; 25728 MW; F22E0AB5 CRC32;

Query Match 20.0%; Score 123; DB 6; Length 235;
Best Local Similarity 35.0%; Pred. No. 2.5e-05;
Matches 35; Conservative 12; Mismatches 39; Indels 14; Gaps 5;

QY 16 PATLSP-----GERATLSCRASOS-VSSNLAWYQKPGQA--PRLLYGASTR--- 62
DB 21 PSFRSPSPDRTNMLDKVLCVLLSNSSGSCWLFORGAASPTFLYISQKPKV 80
QY 63 ATGIPA-RFSGSGSGTEFTLTISSLOSDPAVYCCOQYNN 101
DB 81 ADGLDQRFSGKMGDSFILLDFREEDOGFFCSALSN 120

RESULT 3
P79336 PRELIMINARY; PRT; 210 AA.
AC P79336;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DE CD8 BETA ANTIGEN PRECURSOR.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-THYMUS;
RA MIYAZAWA T.;
RL Submitted (JAN-1997) to the EMBL/genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-THYMUS;
RX MEDLINE; 97067796.
RA PECORARO M.R., SHIMOJIMA M., MAEDA K., INOSHIMA Y., KAWAGUCHI Y.,
RA KAI C., MIKAMI T.;
RT "Molecular cloning of the feline CD8 beta-chain";
RL Immunology 89:84-88(1996).
DR EMBL; AB000484; BAA19125.1; -.
RN [1]
RP SIGNAL.
RP CHAIN 1 21 POTENTIAL.
RP CHAIN 22 210 POTENTIAL.
SQ SEQUENCE 210 AA; 23105 MW; 915E2BD1 CRC32;

Query Match 19.6%; Score 120.5; DB 6; Length 210;
Best Local Similarity 23.7%; Pred. No. 4e-05;
Matches 32; Conservative 25; Mismatches 53; Indels 25; Gaps 5;

QY 1 LMLPDT-----GEIVMTSPATLSPGERATLSCRASOS-VSSNLAWYQKPGQA- 52
DB 5 LMLLATQALRGSSVYVQVNGVINSCEKAKTPTSTRIVLHRRAPSD 64
QY 53 -----RLLYGASTRATGIPARFSGSGTEFTLTISSLOSDPAVYCCOQYNN 100
DB 65 SHVECLAYWDPJKGIVYGGVE-----PEKLIVFPATRIILMLTVKPADSGIVCMYTG 120
QY 101 NMPPTFFGGTKLEI 115
DB 121 S-PELTFEGKTRLSV 134

RESULT 4
Q9Y509 PRELIMINARY; PRT; 147 AA.
AC Q9Y509;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE VH3 PROTEIN (FRAGMENT).
GN VH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96071149.
RA CAO J., VESCOIO R.A., RETTIG M.B., HONG C.H., KIM A., LEE J.C.,
RA LICHTENSTEIN A.K., BERENSON J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple myeloma using PCR with patient-specific immunoglobulin gene primers";
RL Leukemia 9:1948-1953(1995).
DR EMBL; S80860; AAD14339.1; -.
FT NON_TER
SQ SEQUENCE 147 AA; 15768 MW; BDD8E70 CRC32;

Query Match 19.5%; Score 120; DB 4; Length 147;
Best Local Similarity 32.7%; Pred. No. 3e-05;
Matches 37; Conservative 19; Mismatches 39; Indels 18; Gaps 5;
QY 21 VSPGERATLSCRASOSVSS--NLAWYQKPGQA--PRLLYGASTR--ATGIPARFSGS 73
DB 12 VPGKSLRSCASAFSTSTGMSVROAPGKGLMVALISDSQYVYAGSVKRFITIS 71
QY 74 GSGTEFT--LTISLQSDPAVYCCOQYNNMPPT-----FGGTKLEI 115
DB 72 RDNKNTLYLQMTSLRVEDTAVYCAKDGNYFDSVYVYAGIDYVGGCTLYTV 124

RESULT 5
Q9Y4V0 PRELIMINARY; PRT; 397 AA.
AC Q9Y4V0;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE DUS76H24.2 (SIRP-BETA1 (SIGNAL REGULATOR PROTEIN BETA 1)).
GN DUS76H24.2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA MATTHEWS L.;
RL Submitted (JUN-1999) to the EMBL/genbank/DBJ databases.
DR EMBL; AL049634; CAB46661.1; -.
SQ SEQUENCE 397 AA; 43037 MW; C9D81FC5 CRC32;

Query Match 19.1%; Score 117.5; DB 4; Length 397;
Best Local Similarity 24.2%; Pred. No. 0.00017;

Matches 30; Conservative 23; Mismatches 44; Indels 27; Gaps 4;

OY 9 EIVMTOSPATLSVSPGERLTSCRASQSVS-SNLAW-----YQKRGQAPRLI 56
 DB 31 ELQVTPDKSVVAAGESLILHCVTSLIPGPIWFRGAGARELLINQKGEHPRYVT 90
 OY 57 YGASTRATGIPARFGSGSGTEFTLISLQSEDFAVYVCOQYNMWP---YTFGQGT 112
 DB 91 VELTKRNNL-----DFSISINITPADAGTYCVAFRRGSPDVEFKSGAGTE 139
 OY 113 LEIK 116
 DB 140 LSVR 143

RESULT 6
 P78324 PRELIMINARY; PRT; 503 AA.

ID P78324
 AC 01-NOV-1998 (TREMblrel. 08, last sequence update)
 DB 01-NOV-1998 (TREMblrel. 08, last sequence update)
 DE 01-NOV-1999 (TREMblrel. 12, last annotation update)
 DE PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE SUBSTRATE 1 PRECURSOR
 DE (SHP SUBSTRATE-1) (INHIBITORY RECEPTOR SHPS-1) (SIGNAL-
 DE REGULATORY PROTEIN ALPHA-1) (SIRP-ALPHA1) (MYD-1 ANTIGEN).
 GN PTNS1 OR SHPS-1 OR DJ684024.1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE: 97223399.
 RA YAMAO T., MATOZAKI T., AMANO K., MATSUDA Y., TAKAHASHI N., OCHI F.,
 RA "FUTOKA Y., KASUGA M.;
 RT "Mouse and human SHPS-1: molecular cloning of cDNAs and chromosomal
 RT localization of genes."
 RL Biochem. Biophys. Res. Commun. 231:61-67(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RX MEDLINE: 97215901.
 RA KHARITONENKOV A., CHEN Z., SURES I., WANG H., SCHILLING J.,
 RA ULRICH A.;
 RT "A family of proteins that inhibit signalling through tyrosine kinase
 RT receptors."
 RL Nature 386:181-186(1997).
 RN [3]
 RP SEQUENCE OF 146-503 FROM N.A.
 RC BATES K.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: BINDS TO THE SH2 DOMAINS OF PROTEIN-TYROSINE PHOSPHATASE
 CC 2C (SHP-2) AFTER TYROSINE PHOSPHORYLATION INDUCED BY VARIOUS
 CC MITOGENS AND CELL ADHESION. MAY ACT AS A DOCKING PROTEIN AND
 CC INDUCE TRANSLLOCATION OF SHP-2 FROM THE CYTOSOL TO THE PLASMA
 CC MEMBRANE.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN BRAIN.
 CC HIGH LEVELS ALSO PRESENT IN HEART, SPLEEN, TESTIS, OVARY AND
 CC PERIPHERAL BLOOD LEUKOCYTES.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC TWO C1-LIKE AND ONE V-LIKE DOMAINS.
 DR EMBL: D86043; BAA12974.1; -;
 DR EMBL: Y10375; CAW71403.1; -;
 DR EMBL: AL034362; CAB38874.1; -;
 DR MIM: 602461; -;
 DR PFMW: PF00047; 16; 3.
 KW Signal; Transmembrane; Alternative splicing; Immunoglobulin domain;
 KW Glycoprotein; SH3-binding; Phosphorylation.
 FT SIGNAL 1 26
 FT CHAIN 27 503
 FT DOMAIN 27 372
 FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 373 393 POTENTIAL.
 FT DOMAIN 394 503 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 43 129 IG-LIKE V-TYPE DOMAIN.
 FT DOMAIN 164 233 IG-LIKE C1-TYPE DOMAIN.
 FT DOMAIN 266 339 IG-LIKE C1-TYPE DOMAIN.
 FT DOMAIN 428 431 SH2-BINDING (POTENTIAL).
 FT DOMAIN 438 443 SH3-BINDING (POTENTIAL).
 FT DOMAIN 452 455 SH2-BINDING (POTENTIAL).
 FT DOMAIN 469 472 SH2-BINDING (POTENTIAL).
 FT DOMAIN 495 498 SH2-BINDING (POTENTIAL).
 FT MOD_RES 428 428 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 452 452 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 469 469 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RES 495 495 PHOSPHORYLATION (POTENTIAL).
 FT CARBOHYD 244 244 POTENTIAL.
 FT CARBOHYD 269 269 POTENTIAL.
 FT CARBOHYD 291 291 POTENTIAL.
 FT CARBOHYD 318 318 POTENTIAL.
 SQ SEQUENCE 503 AA; 54812 MW; 0CA5272E CRC32;

Query Match 19.0%; Score 117; DB 4; Length 503;
 Best Local Similarity 24.4%; Pred. No. 0.00025;
 Matches 30; Conservative 23; Mismatches 44; Indels 26; Gaps 4;

OY 9 EIVMTOSPATLSVSPGERLTSCRASQSVS-SNLAW-----YQKRGQAPRLI 56
 DB 33 ELQVTPDKSVVAAGESLILHCVTSLIPGPIWFRGAGARELLINQKGEHPRYVT 92
 OY 57 YGASTRATGIPARFGSGSGTEFTLISLQSEDFAVYVCOQYNMWP---YTFGQGT 113
 DB 93 VESTKRENN-----DFSISINITPADAGTYCVAFRRGSPDTEKSGAGTEL 141
 OY 114 LEIK 116
 DB 142 SVR 144

RESULT 7
 000241 PRELIMINARY; PRT; 398 AA.

ID 000241
 AC 000241;
 DT 01-NOV-1998 (TREMblrel. 08, last sequence update)
 DT 01-NOV-1998 (TREMblrel. 08, last sequence update)
 DE 01-NOV-1999 (TREMblrel. 11, last annotation update)
 DE SIGNAL-REGULATORY PROTEIN BETA-1 PRECURSOR (SIRP-BETA1).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RA KHARITONENKOV A., CHEN Z., SURES I., WANG H., SCHILLING J.,
 RA ULRICH A.;
 RL Nature 386:181-186(1997).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC TWO C1-LIKE AND ONE V-LIKE DOMAINS.
 DR EMBL: Y10376; CAW71404.1; -;
 DR PFMW: PF00047; 16; 3.
 KW Signal; Immunoglobulin domain; Glycoprotein; Transmembrane.
 FT SIGNAL 1 26
 FT CHAIN 27 398
 FT DOMAIN 27 371
 FT DOMAIN 372 392
 FT TRANSMEM 372 392
 FT DOMAIN 393 398
 FT DOMAIN 42 128
 FT DOMAIN 163 233
 FT DOMAIN 267 338
 FT CARBOHYD 102 102
 FT CARBOHYD 244 244
 FT CARBOHYD 269 269
 FT CARBOHYD 291 291
 FT SIGNAL 291 291
 FT EXTRACELLULAR (POTENTIAL).
 FT SIGNAL-REGULATORY PROTEIN BETA-1.
 FT POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT IG-LIKE V-TYPE DOMAIN.
 FT IG-LIKE C1-TYPE DOMAIN.
 FT IG-LIKE C1-TYPE DOMAIN.
 FT IG-LIKE C1-TYPE DOMAIN.
 FT POTENTIAL.
 FT POTENTIAL.
 FT POTENTIAL.
 FT POTENTIAL.

SEQUENCE 398 AA; 43254 MW; 185877D0 CRC32;

Query Match

Best Local Similarity 18.8%; Score 115.5; DB 4; Length 398;
Matches 30; Conservative 22; Mismatches 45; Indels 27; Gaps 4;

9 EIVTOSPATLSVSPGERATLSGCRASQSVS-SNLAW-----YQKPGQAPRLI 56
Db 32 ELQYIOPEKSVSVAAGEBATLRCANTSLIPGPIWFGAGAGRELLYNQKEGHEPRVTT 91

57 YGASTRATGIPARFSGSGTEFTLTSSLOSEDFAVYCCOQYNNWP-----YTFGQGT 112
Db 92 VSELTNRNLT-----NFSISISNITPADAGTYCYKFRGSDPDVEFRSGAGTE 140

113 LEIR 116

141 LSVR 144

RESULT 8

09XSM7 PRELIMINARY; PRT; 209 AA.

01-NOV-1999 (Tremblrel. 12, Created)

01-NOV-1999 (Tremblrel. 12, Last sequence update)

01-NOV-1999 (Tremblrel. 12, Last annotation update)

01-NOV-1999 (Tremblrel. 12, Last annotation update)

01-NOV-1999 (Tremblrel. 12, Last annotation update)

01-NOV-1999 (Tremblrel. 12, Last annotation update)

01-NOV-1999 (Tremblrel. 12, Last annotation update)

01-NOV-1999 (Tremblrel. 12, Last annotation update)

01-NOV-1999 (Tremblrel. 12, Last annotation update)

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01-NOV-1999 (Tremblrel. 12, Last annotation update)

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01-NOV-1999 (Tremblrel. 12, Last annotation update)

01-NOV-1999 (Tremblrel. 12, Last annotation update)

01-NOV-1999 (Tremblrel. 12, Last annotation update)

01-NOV-1999 (Tremblrel. 12, Last annotation update)

SEQUENCE 118 AA; 13036 MW; 45653221 CRC32;

Query Match

Best Local Similarity 17.8%; Score 109.5; DB 11; Length 118;
Matches 39; Conservative 17; Mismatches 44; Indels 23; Gaps 7;

9 EIVTOSPATLSVSPGERATLSGCRAS--QSVSNLAWYQKPGQAPRLI--YTGASTRAT 64
Db 1 QVYQSGAELA-RPMASVKLSKASGYNFNSYMWQKORPGGLEMGALY-PGDDT 58

65 GIPARFSGSG-----SGTEFTLTSSLOSEDFAVYCCOQ-----YNNPPTTFGQGT 112
Db 59 SYTGKFRGKATLADKSSSTAYMOLSLASEDSAVYCCARTVGGYEDYV-----GGGT 113

113 LEI 115

114 LTV 116

RESULT 10

09YHR9 PRELIMINARY; PRT; 136 AA.

01-MAY-1999 (Tremblrel. 10, Created)

01-MAY-1999 (Tremblrel. 10, Last sequence update)

01-MAY-1999 (Tremblrel. 10, Last annotation update)

01-MAY-1999 (Tremblrel. 10, Last annotation update)

01-MAY-1999 (Tremblrel. 10, Last annotation update)

01-MAY-1999 (Tremblrel. 10, Last annotation update)

01-MAY-1999 (Tremblrel. 10, Last annotation update)

01-MAY-1999 (Tremblrel. 10, Last annotation update)

01-MAY-1999 (Tremblrel. 10, Last annotation update)

01-MAY-1999 (Tremblrel. 10, Last annotation update)

01-MAY-1999 (Tremblrel. 10, Last annotation update)

01-MAY-1999 (Tremblrel. 10, Last annotation update)

01-MAY-1999 (Tremblrel. 10, Last annotation update)

01-MAY-1999 (Tremblrel. 10, Last annotation update)

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01-MAY-1999 (Tremblrel. 10, Last annotation update)

01-MAY-1999 (Tremblrel. 10, Last annotation update)

01-MAY-1999 (Tremblrel. 10, Last annotation update)

SEQUENCE 136 AA; 14871 MW; 0383152C CRC32;

Query Match

Best Local Similarity 17.6%; Score 108.5; DB 13; Length 136;
Matches 34; Conservative 15; Mismatches 47; Indels 15; Gaps 4;

14 QSPATLSVSPGERATLSGCRASQSVS-SNLAWYQKPGQAPRLIYGASTRATGIPARF 71
Db 2 QPTTIRKAGESLTINCVARDSCALSSYVYRKSGSNNEI---SGGKRYEIVNS 58

72 GSGSGTEFTLTSSLOSEDFAVYCCOQYNNW-----PYTFGQGTLEI 115
Db 59 GSKS---FSIRINDLEDESGYRCKLGLWMCDELDELDEYGGVTVV 106

RESULT 11

077624 PRELIMINARY; PRT; 100 AA.

01-MAY-1999 (Tremblrel. 10, Created)

01-MAY-1999 (Tremblrel. 10, Last sequence update)

01-MAY-1999 (Tremblrel. 10, Last annotation update)

01-MAY-1999 (Tremblrel. 10, Last annotation update)

01-MAY-1999 (Tremblrel. 10, Last annotation update)

01-MAY-1999 (Tremblrel. 10, Last annotation update)

01-MAY-1999 (Tremblrel. 10, Last annotation update)

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01-MAY-1999 (Tremblrel. 10, Last annotation update)

01-MAY-1999 (Tremblrel. 10, Last annotation update)


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DE 01-NOV-1998 (TREMblrel. 08, Created)
DT 01-NOV-1998 (TREMblrel. 08, last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, last annotation update)
DE SURROGATE LIGHT CHAIN (FRAGMENT).
GN VPREB.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BONE MARROW.
RA RAYCHEL A.P., HALLIGAN B.D.;
RL Raychell A.P., Halligan B.D.;
DR EMBL; AF068846; AAC19380.1; -.
DR HSSP; P01703; 7FAB.
FT NON_TER 1
FT SIGNAL 1
SO SEQUENCE 100 AA; 11142 MW; 3785537C CRC32;

Query Match
Best Local Similarity 36.8%; Pred. No. 0.00033;
Matches 32; Conservative 13; Mismatches 32; Indels 10; Gaps 5;

OY 11 VMTQSPATLSVSPGERATLSCRASQSVSSNL---AWYQKPGQAPRLI--YGASTPATG 65
DB 15 VLSQPSVAVSFL-GATVRLACTLSSDHVNLHSITWQKRGHRPRLNLFSPSDKROG 73
OY 66 --IPARFSGSGSGTEFT--LTISLSOS 88
DB 74 HKVPRFSGSKDLAKNTGYSLNELQA 100

RESULT 12
OY298 PRELIMINARY; PRT; 150 AA.
AC Q9Y298;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, last sequence update)
DT 01-NOV-1999 (TREMblrel. 12, last annotation update)
DE IGG VH PROTEIN PRECURSOR (FRAGMENT).
GN IGG VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE; 96322155.
RA JACQUEMIN M.G., VANDER ELST L.P.L.;
RT "Mechanism and kinetics of factor VIII inactivation: study with an
RT 1964 monoclonal antibody derived from a hemophilia A patient with
RT inhibitor."
RL Blood 92:496-506(1998).
DR EMBL; AJ224083; CA11829.1; -.
GN EMBL;
FT SIGNAL 1
FT NON_TER 150
FT POTENTIAL.
SO SEQUENCE 150 AA; 16031 MW; B18C39A CRC32;

Query Match
Best Local Similarity 32.5%; Pred. No. 0.00067;
Matches 41; Conservative 18; Mismatches 43; Indels 24; Gaps 8;

OY 6 TGEIWTQSPATLSVSPGERATLSCRASQSVSSNL--WYQKPGQAPRLIYGASTRA 63
DB 17 THAQVLYVQSGAEV-KPGASVYKSCVSGYTLTELPVHWGAPKRG--LEWVGSPDPE 73
OY 64 TG--IAR-SSGSGSGTEFTL-----ISSLSQSDPAVYCC-----QQYNNPPTFFGQ 109
DB 74 SGEIYAREFGSVTWTADISTDIAYWELSSLSDDPAVYCAVPDPADWDI--GQ 128

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OY 110 GFKLEI 115
DB 129 GIMVTV 134

RESULT 13
O46631 PRELIMINARY; PRT; 506 AA.
AC O46631;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, last sequence update)
DT 01-MAY-1999 (TREMblrel. 10, last annotation update)
DE MYD-1 ANTIGEN PRECURSOR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PERIPHERAL BLOOD;
RX MEDLINE; 96143722.
RA BROOKE G.P., PARSONS K.R., HOWARD C.J.;
RT "Cloning of two members of the SIRP alpha family of protein tyrosine
RT phosphatase binding proteins in cattle that are expressed on monocytes
RT and a subpopulation of dendritic cells and which mediate binding to
RT CD4 T cells."
RL Eur. J. Immunol. 28:1-11(1998).
DR EMBL; Y11046; CAA1943.1; -.
DR PFAM; PF00047; 19; 3.
FT SIGNAL 1
FT CHAIN 27
FT POTENTIAL.
FT MYD-1 ANTIGEN.
SO SEQUENCE 506 AA; 55092 MW; 3D320629 CRC32;

Query Match
Best Local Similarity 25.8%; Pred. No. 0.0039;
Matches 32; Conservative 19; Mismatches 46; Indels 27; Gaps 4;

OY 8 GEIVTQSPATLSVSPGERATLSCRA-SQSVSSNLAM-----YQKPGQAPRL 55
DB 32 GEIVTQSPATLSVSPGERATLSCRA-SQSVSSNLAM-----YQKPGQAPRL 55
OY 56 IYGASTRATGIPARFSGSGTEFTLISLQSDPAVYCCQYNNP---PYTGQGT 111
DB 92 NVSDATKRNMM-----DFSIRISNTPADAGVYCVAFRRERGDMEKSGPGT 140
OY 112 KLEI 115
DB 141 HLTIV 144

RESULT 14
O70153 PRELIMINARY; PRT; 228 AA.
AC O70153;
DT 01-AUG-1998 (TREMblrel. 07, Created)
DT 01-AUG-1998 (TREMblrel. 07, last sequence update)
DT 01-MAY-1999 (TREMblrel. 10, last annotation update)
DE B29/IG-BETA/CD79B.
GN B29/IG-BETA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MISTAR; TISSUE-BRAIN;
RX MEDLINE; 96207252.
RA NAKAZATO S., NOMOTO K., KAZAHARI K., ONO M.;
RT "Physical linkage of the B29/Ig-beta (CD79B) gene to the skeletal
RT muscle, sodium-channel, and growth hormone genes in rat and human."
RL Genomics 48:363-368(1998).
DR EMBL; AB004831; BAA25652.1; -.

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